

Human Nucleic Acid Sequences from Ovarian Tumor Tissue

The invention relates to human nucleic acid sequences from ovarian tumor tissue, which code for gene products or parts thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main cancer causes of death in women is ovarian cancer, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

A database that consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue. ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer (> 2000 nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified that are important for tumor formation and proliferation. There is, however, the following problem: Since the EST sequences that are found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this error possibility can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID Nos. 1-123 and 258-273, which play a role as candidate genes in ovarian cancer, have now been found.

Nucleic acid sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a part thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 or a complementary or allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID Nos. 1-123 and 258-273, which are expressed elevated in ovarian tumor tissue.

The invention also relates to nucleic acid sequences Seq. ID Nos. 27, 32, 42, 46, 67, 76, 78, 80, 85, 88, 90, 108, and 112, which are expressed elevated in breast tumor tissue.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs, ϕ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia), 2. eukaryotic, such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

A control or regulatory sequence is defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P_R, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The genes that can be obtained are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as E. coli or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides according to the sequence protocols Seq. ID Nos. 124-257 and 274-307.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of Seq. ID Nos. 124-257 and 274-307 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID Nos. 1-123 and 258-273.

Antibodies are defined especially as monoclonal antibodies.

The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The invention also relates to phage-display phages, which are directed against a polypeptide or a fragment and which are coded by the nucleic acids of sequences Seq. ID Nos. 1-123 and 258-273 according to the invention.

The polypeptides of sequences Seq. ID Nos. 124-257 and 274-305 according to the invention can also be used as tools for finding active ingredients against ovarian cancer, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID Nos. 1-123 and 258-273 for expression of polypeptides, which can be used as tools for finding active ingredients against ovarian cancer.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID Nos. 124-257 and 274-305 as pharmaceutical agents in the gene therapy for treatment of ovarian cancer or for the production of a pharmaceutical agent for treatment of ovarian cancer.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID Nos. 124-257 and 274-305.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained from cDNAs of sequences Seq. ID Nos. 1-123 and 258-273, and their use together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences), genomic BAC, PAC and Cosmid libraries are screened and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and Cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and Cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and Cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-123 and 258-273 for use as vehicles for gene transfer.

Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes).

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence.

Contig = A set of DNA sequences that can be combined as a result of very great similarities into one sequence (consensus).

Singleton = A contig that contains only one sequence.

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in various proteins.

N = selectively the nucleotide A, T, G or C.

X = selectively one of the 20 naturally occurring amino acids.

Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area

maximum pads per read = maximum number of insertions

maximum percent mismatch = maximum deviation in %

Explanation of Figures

Figure 1 shows the systematic gene search in the Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

- Figure 3 shows the in-silico subtraction of gene expression in various tissues
- Figure 4a shows the determination of tissue-specific expression via electronic Northern
- Figure 4b shows the electronic Northern
- Figure 5 shows the isolation of genomic BAC and PAC clones.

The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

Example 1

Search for tumor-related candidate genes

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

Figures 2b1-2b4 illustrate the lengthening of the ovarian tumor tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another).

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

Example 2**Algorithm for identification and lengthening of partial cDNA sequences with altered expression pattern**

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

2.1. Electronic Northern Blot

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blots.

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 68 was found which occurs 6.08 x more heavily in normal ovarian tissue than in tumor tissue.

The result is as follows:

Electronic Northern for SEQ. ID NO.: 68

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0179	1.0896	0.9178
Breast	0.0141	0.0244	0.5758	1.7366
Small intestine	0.0184	0.0165	1.1122	0.8991
Ovary	0.0030	0.0182	0.1645	6.0803
Endocrine tissue	0.0136	0.0226	0.6038	1.6562
Gastrointestinal	0.0211	0.0185	1.1390	0.8780
Brain	0.0126	0.0082	1.5299	0.6536
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0110	0.0847	0.1300	7.6946
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0233	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0062	0.0143	0.4355	2.2964
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0066	0.0055	1.1966	0.8357
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0153	0.0043	3.5827	0.2791
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0384			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0147			
Cervix	0.0426			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0178	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0259
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0040
Placenta	0.0121	Nerves	0.0479
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

[illegible]

The result is as follows:

Electronic Northern for SEQ. ID NO.: 86

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0128	0.9153	1.0926
Breast	0.0090	0.0169	0.5293	1.8893
Small intestine	0.0092	0.0331	0.2781	3.5964
Ovary	0.0030	0.0234	0.1279	7.8175
Endocrine tissue	0.0204	0.0426	0.4795	2.0856
Gastrointestinal	0.0211	0.0185	1.1390	0.8780
Brain	0.0274	0.0195	1.4020	0.7133
Hematopoietic	0.0107	0.1136	0.0941	10.6267
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0307	0.0137	2.2358	0.4473
Testicles	0.0115	0.0819	0.1406	7.1142
Lung	0.0104	0.0286	0.3629	2.7557
Lung	0.0290	0.0153	1.8908	0.5289
Stomach-esophagus	0.0188	0.0300	0.6282	1.5918
Muscle-skeleton	0.0163	0.0342	0.4758	2.1016
Kidney	0.0132	0.0110	1.1966	0.8357
Pancreas	0.0150	0.0000	undef	0.0000
Penis	0.0174	0.0234	0.7445	1.3433
Prostate	0.0270	0.5277	0.0512	19.5264
Uterus-endometrium	0.0229	0.0408	0.5611	1.7821
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0160			
Breast hyperplasia	0.0297			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0353			
Sensory organs	0.0095			
White blood cells	0.0106			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0245
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0097
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0010
Placenta	Nerves 0.0000
Prostate	Prostate 0.0155
Sensory organs	Sensory Organs 0.0000
	Uterus_n

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 114 was found which occurs 6.94 x more heavily in normal ovarian tissue than in tumor tissue.

The result is as follows:

Electronic Northern for SEQ. ID NO.: 114

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0117	0.0026	4.5763	0.2185
Small intestine	0.0026	0.0075	0.3403	2.9389
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0208	0.1439	6.9489
Gastrointestinal	0.0085	0.0025	3.3962	0.2944
Brain	0.0057	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0083	0.0102	0.8129	1.2302
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0136	0.0000	undef	0.0000
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0065	0.0064	1.0236	0.9769
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0305	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0445			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0213			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	
Gastrointestinal	0.0000	Ovary_n	0.0136
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.1418
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0047
Heart-blood vessels	0.0000	Hematopoietic	0.0244
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0154
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0137
		Uterus_n	0.0000

In an analogous procedure, the following Northernblots were also found:

Electronic Northern for SEQ. ID NO.: 1

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0077	1.0170	0.9833
Breast	0.0179	0.0075	2.3818	0.4198
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0120	0.0364	0.3289	3.0402
Endocrine tissue	0.0119	0.0100	1.1887	0.8413
Gastrointestinal	0.0134	0.0139	0.9664	1.0348
Brain	0.0059	0.0103	0.5760	1.7362
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0095	0.0129	0.7353	1.3600
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0000	0.0351	0.0000	undef
Lung	0.0052	0.0164	0.3175	3.1494
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0120	0.0120	0.9994	1.0006
Kidney	0.0109	0.0068	1.5861	0.6305
Pancreas	0.0017	0.0110	0.1496	6.6857
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0061			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0136
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0245
Skin	Fetal 0.0070
Hepatic	Gastrointestinal 0.0122
Heart-blood vessels	Hematopoietic 0.0057
Lung	Skin-muscle 0.0032
Suprarenal gland	Testicles 0.0154
Kidney	Lung 0.0164
Placenta	Nerves 0.0141
Prostate	Nerves 0.0205
Sensory organs	Prostate 0.0000
	Sensory Organs 0.0083
	Uterus_n

Electronic Northern for SEQ. ID NO.: 2

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0031	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency	% frequency	
Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0171
Lung	0.0000	Skin-muscle	0.0194
Suprarenal gland	0.0000	Testicles	0.0082
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0137
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 3

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0026	4.5763	0.2185
Breast	0.0064	0.0019	3.4026	0.2939
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0034	0.0075	0.4528	2.2083
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0085	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0051	0.1908	0.0267	37.4714
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0071	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0062	Lung	0.0164
Placenta	0.0000	Nerves	0.0000
Prostate	0.0061	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 4

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000 undef	
Small intestine	0.0051	0.0000	undef 0.0000	
Ovary	0.0000	0.0000	undef undef	
Endocrine tissue	0.0000	0.0572	0.0000 undef	
Gastrointestinal	0.0034	0.0075	0.4528 2.2083	
Brain	0.0019	0.0093	0.2071 4.8289	
Hematopoietic	0.0022	0.0021	1.0799 0.9260	
Skin	0.0013	0.0379	0.0353 28.3379	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0000	0.0065	0.0000 undef	
Testicles	0.0053	0.0000	undef 0.0000	
Lung	0.0000	0.0000	undef undef	
Stomach-esophagus	0.0104	0.0041	2.5402 0.3937	
Muscle-skeleton	0.0000	0.0000	undef undef	
Kidney	0.0017	0.0000	undef 0.0000	
Pancreas	0.0027	0.0000	undef 0.0000	
Penis	0.0083	0.0000	undef 0.0000	
Prostate	0.0030	0.0000	undef 0.0000	
Uterus-endometrium	0.0022	0.0000	undef 0.0000	
Uterus-myometrium	0.0000	0.0000	undef undef	
Uterus-general	0.0051	0.0000	undef 0.0000	
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0035			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0093
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0142	Skin-muscle	0.0065
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0062	Nerves	0.0060
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0208
	0.0251	Uterus_n	

Electronic Northern for SEQ. ID NO.: 5

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0130	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0012
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n

Electronic Northern for SEQ. ID NO.: 6

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0128	0.3051	3.2777
Breast	0.0141	0.0075	1.8715	0.5343
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0120	0.0390	0.3070	3.2573
Endocrine tissue	0.0290	0.0376	0.7698	1.2990
Gastrointestinal	0.0211	0.0324	0.6508	1.5365
Brain	0.0126	0.0144	0.8742	1.1439
Hematopoietic	0.0174	0.0000	undef	0.0000
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0218	0.0204	1.0669	0.9373
Stomach-esophagus	0.0193	0.0153	1.2605	0.7933
Muscle-skeleton	0.0137	0.0000	undef	0.0000
Kidney	0.0190	0.0205	0.9252	1.0808
Pancreas	0.0099	0.0110	0.8974	1.1143
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0109	0.0106	1.0236	0.9769
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0408	0.3741	2.6732
Uterus-general	0.0306	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0217			
Cervix	0.0319			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0476
Gastrointestinal	0.0557	Ovary_n	0.3190
Brain	0.0167	Ovary_t	0.0101
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0151
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0213	Skin-muscle	0.0000
Suprarenal gland	0.0181	Testicles	0.0309
Kidney	0.0254	Lung	0.0082
Placenta	0.0185	Nerves	0.0010
Prostate	0.0121	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0310
	0.0251	Uterus_n	0.0458

Electronic Northern for SEQ. ID NO.: 7

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0077	0.0000 undef	
Breast	0.0026	0.0113	0.2268 4.4083	
Small intestine	0.0031	0.0331	0.0927 10.7893	
Ovary	0.0000	0.0182	0.0000 undef	
Endocrine tissue	0.0051	0.0050	1.0189 0.9815	
Gastrointestinal	0.0057	0.0139	0.4142 2.4145	
Brain	0.0030	0.0010	2.8798 0.3472	
Hematopoietic	0.0027	0.0000	undef 0.0000	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0000	0.0065	0.0000 undef	
Heart	0.0000	0.0000	undef undef	
Testicles	0.0062	0.0123	0.5080 1.9684	
Lung	0.0000	0.0000	undef undef	
Stomach-esophagus	0.0000	0.0000	undef undef	
Muscle-skeleton	0.0163	0.0205	0.7930 1.2610	
Kidney	0.0017	0.0055	0.2991 3.3428	
Pancreas	0.0030	0.0000	undef 0.0000	
Penis	0.0000	0.0021	0.0000 undef	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0064			
Uterus-general	0.0030			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0106			
White blood cells				
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0072	Testicles	0.0000
Kidney	0.0000	Lung	0.0120
Placenta	0.0000	Nerves	0.0205
Prostate	0.0000	Prostate	0.0077
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0064	0.0038	1.7013	0.5878	
Small intestine	0.0031	0.0000	undef	0.0000	
Ovary	0.0000	0.0156	0.0000	undef	
Endocrine tissue	0.0068	0.0125	0.5434	1.8403	
Gastrointestinal	0.0000	0.0046	0.0000	undef	
Brain	0.0037	0.0000	undef	0.0000	
Hematopoietic	0.0027	0.0000	undef	0.0000	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0065	0.0000	undef	
Heart	0.0042	0.0137	0.3084	3.2426	
Testicles	0.0058	0.0000	undef	0.0000	
Lung	0.0031	0.0000	undef	0.0000	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0060	0.0000	undef	
Muscle-skeleton	0.0054	0.0068	0.7930	1.2610	
Kidney	0.0050	0.0000	undef	0.0000	
Pancreas	0.0120	0.0000	undef	0.0000	
Penis	0.0022	0.0000	undef	0.0000	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0000	0.0068	0.0000	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0089				
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0118				
Seminal vesicle	0.0026				
Sensory organs	0.0000				
White blood cells					
Cervix					

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0111
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0020
Placenta	0.0061	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0333
		Uterus_n	

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0034	0.0201	0.1698	5.8889
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0081	0.0072	1.1314	0.8839
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0010	0.0020	0.5080	1.9684
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0051	0.0000	undef	0.0000
Muscle-skeleton	0.0054	0.0000	undef	0.0000
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0065	0.0043	1.5354	0.6513
Prostate	0.0068	0.1583	0.0427	23.4317
Prostate	0.0152	0.0000	undef	0.0000
Uterus-endometrium	0.0051	0.0000	undef	0.0000
Uterus-myometrium	0.0096			
Uterus-general	0.0149			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0093
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0309
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0100
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 10

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0009			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0000

Electronic Northern for SEQ. ID NO.: 12

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0026	6.1018	0.1639
Breast	0.0102	0.0038	2.7221	0.3674
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0170	0.0201	0.8491	1.1778
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0126	0.0072	1.7485	0.5719
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0093	0.0061	1.5241	0.6561
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0137	0.0180	0.7615	1.3133
Kidney	0.0054	0.0479	0.1133	8.8268
Pancreas	0.0083	0.0055	1.4957	0.6686
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0087	0.0021	4.0945	0.2442
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0381	0.0068	5.6113	0.1782
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0095			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal		Ovary_n	0.0000
Brain	0.0139	Ovary_t	0.0000
Hematopoietic	0.0083	Endocrine tissue	0.0000
Skin	0.0063	Fetal	0.0082
Hepatic	0.0118	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0107	Skin-muscle	0.0259
Suprarenal gland	0.0072	Testicles	0.0154
Kidney	0.0000	Lung	0.0082
Placenta	0.0247	Nerves	0.0040
Prostate	0.0182	Prostate	0.0205
Sensory organs	0.0249	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 13

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0055	0.0000	undef
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0044	0.0021	2.0473	0.4885
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0235	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix	0.0000	0.0000	undef	undef

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0077
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 15

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0051	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0086	0.0120	0.7139	1.4008
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0087	0.0064	1.3648	0.7327
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0059			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0035			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0057
Heart-blood vessels	0.0072	Hematopoietic	0.0032
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0061	Lung	0.0010
Placenta	0.0000	Nerves	0.0137
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 16

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0179	0.6538	1.5296
Breast	0.0307	0.0226	1.3611	0.7347
Small intestine	0.0215	0.0000	undef	0.0000
Ovary	0.0090	0.0338	0.2657	3.7640
Endocrine tissue	0.0034	0.0050	0.6792	1.4722
Gastrointestinal	0.0192	0.0185	1.0354	0.9658
Brain	0.0074	0.0133	0.5538	1.8057
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0257	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0148	0.0137	1.0794	0.9265
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0353	0.0164	2.1591	0.4631
Stomach-esophagus	0.0387	0.0077	5.0421	0.1983
Muscle-skeleton	0.0154	0.0120	1.2850	0.7782
Kidney	0.0163	0.0274	0.5948	1.6813
Pancreas	0.0198	0.0166	1.1966	0.8357
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0196	0.0064	3.0709	0.3256
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0384			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0178			
Sensory organs	0.0353			
White blood cells	0.0182			
Cervix	0.0426			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0136
Gastrointestinal	0.0056	Ovary_n	0.1595
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0249	Hematopoietic	0.0114
Lung	0.0181	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0164
Placenta	0.0061	Nerves	0.0110
Prostate	0.0499	Prostate	0.0274
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0458

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0030	0.0234	0.1279	7.8175
Endocrine tissue	0.0000	0.0125	0.0000	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0044	0.0021	2.1599	0.4630
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0104	0.0041	2.5402	0.3937
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0083	0.0000	undef	0.0000
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0096			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0017			
Sensory organs	0.0319			
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0203
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0128
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0259
Lung	0.0036	Skin-muscle	0.0077
Suprarenal gland	0.0000	Testicles	0.0164
Kidney	0.0062	Lung	0.0100
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0251	Sensory Organs	0.0333
		Uterus_n	

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0020	0.0000	undef
Lung	0.0000	0.0077	0.0000	undef
Stomach-esophagus	0.0051	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0022	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0065
Lung	0.0000	Skin-muscle	0.0077
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 20

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0030	0.0021	1.4399	0.6945
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0137	0.2313	4.3235
Testicles	0.0000	0.0000	undef	undef
Lung	0.0073	0.0020	3.5562	0.2812
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0050	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0044	0.0021	2.0473	0.4885
Prostate	0.0068	0.0000	undef	0.0000
Uterus-endometrium	0.0076	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0061			
White blood cells	0.0000			
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0171
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0155
Sensory organs		Sensory Organs	0.0000
		Uterus n	

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0165	0.0000	undef
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0068	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0051	0.0019	2.7221	0.3674
Small intestine	0.0031	0.0331	0.0927	10.7893
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0034	0.0100	0.3396	2.9444
Gastrointestinal	0.0096	0.0093	1.0354	0.9658
Brain	0.0059	0.0021	2.8798	0.3472
Hematopoietic	0.0000	0.0379	0.0000	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0061	0.6774	1.4763
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0027	0.0137	0.1983	5.0439
Pancreas	0.0099	0.0055	1.7949	0.5571
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064	0.0000	0.0059	0.0000
Prostate hyperplasia	0.0059	0.0000	0.0000	0.0000
Seminal vesicle	0.0000	0.0017	0.0017	0.0000
Sensory organs	0.0000	0.0000	0.0000	0.0000
White blood cells	0.0000	0.0000	0.0000	0.0000
Cervix	0.0000	0.0000	0.0000	0.0000

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0195	0.0077	2.5424	0.3933
Breast	0.0064	0.0075	0.8507	1.1756
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0153	0.0226	0.6792	1.4722
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0081	0.0092	0.8800	1.1364
Hematopoietic	0.0067	0.0379	0.1764	5.6676
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0083	0.0102	0.8129	1.2302
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0103	0.0180	0.5711	1.7510
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0329	0.0000	undef	0.0000
Prostate	0.0153	0.0064	2.3885	0.4187
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0305	0.0136	2.2445	0.4455
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0069			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0139	Breast	0.0136
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0157	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0099
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0171
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0060
Placenta	0.0121	Nerves	0.0205
Prostate	0.0249	Prostate	0.0387
Sensory organs	0.0000	Sensory Organs	0.0250
		Uterus_n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0204	0.1907	5.2444
Breast	0.0141	0.0263	0.5347	1.8702
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0090	0.0312	0.2878	3.4745
Endocrine tissue	0.0136	0.0150	0.9057	1.1042
Gastrointestinal	0.0192	0.0185	1.0354	0.9658
Brain	0.0222	0.0113	1.9635	0.5093
Hematopoietic	0.0094	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0129	0.3676	2.7200
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0135	0.0123	1.1007	0.9085
Stomach-esophagus	0.0097	0.0153	0.6303	1.5866
Muscle-skeleton	0.0188	0.0300	0.6282	1.5918
Kidney	0.0163	0.0205	0.7930	1.2610
Pancreas	0.0083	0.0221	0.3739	2.6743
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0109	0.0043	2.5591	0.3908
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0204	0.3741	2.6732
Uterus-general	0.0102	0.0954	0.1067	9.3678
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0089			
Sensory organs	0.0235			
White blood cells	0.0087			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.1595
Brain	0.0111	Ovary_t	0.0203
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0058
Hepatic	0.0000	Gastrointestinal	0.0488
Heart-blood vessels	0.0260	Hematopoietic	0.0114
Lung	0.0107	Skin-muscle	0.0032
Suprarenal gland	0.0072	Testicles	0.0154
Kidney	0.0000	Lung	0.0164
Placenta	0.0124	Nerves	0.0060
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0234	0.0204	1.1441	0.8741
Breast	0.0192	0.0470	0.4083	2.4491
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0090	0.0546	0.1645	6.0803
Endocrine tissue	0.0204	0.0075	2.7170	0.3681
Gastrointestinal	0.0268	0.0416	0.6443	1.5522
Brain	0.0037	0.0154	0.2400	4.1669
Hematopoietic	0.0147	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0476	0.0259	1.8382	0.5440
Heart	0.0095	0.0412	0.2313	4.3235
Testicles	0.0000	0.0000	undef	undef
Lung	0.0166	0.0184	0.9032	1.1072
Stomach-esophagus	0.0387	0.0460	0.8404	1.1900
Muscle-skeleton	0.0069	0.0300	0.2284	4.3775
Kidney	0.0543	0.0411	1.3217	0.7566
Pancreas	0.0363	0.0110	3.2906	0.3039
Penis	0.0060	0.0267	0.2246	4.4517
Prostate	0.0218	0.0128	1.7060	0.5862
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0352			
Prostate hyperplasia	0.0535			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0078			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0204
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0040
Placenta	0.0121	Nerves	0.0137
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 27

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0074	0.0051	1.4399	0.6945
Hematopoietic	0.0027	0.0379	0.0706	14.1689
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0022	0.0128	0.1706	5.8615
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0235			
Seminal vesicle	0.0017			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0000
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0090	0.0038	2.3818	0.4198
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0119	0.0100	1.1887	0.8413
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0015	0.0031	0.4800	2.0835
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0041	0.2540	3.9367
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0034	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0109	0.0043	2.5591	0.3908
Prostate	0.0068	0.0528	0.1280	7.8106
Prostate	0.0000	0.0136	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0059			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0213			
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0039	Endocrine tissue	0.0076
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0032
Lung	0.0217	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0030
Placenta	0.0121	Nerves	0.0137
Prostate	0.0000	Prostate	0.0000
	0.0000	Sensory Organs	0.0000
Sensory organs		Uterus n	

Electronic Northern for SEQ. ID NO.: 29

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0020	0.5080	1.9684
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0021	0.0000	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0051	0.0000	undef	0.0000
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0009			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0032
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 30

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0026	3.0509	0.3278
Breast	0.0038	0.0113	0.3403	2.9389
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0030	0.0702	0.0426	23.4526
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0556	0.0278	2.0018	0.4995
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0323	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0062	0.0082	0.7621	1.3122
Lung	0.0097	0.0077	1.2605	0.7933
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0110	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0065	0.0255	0.2559	3.9077
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0192			
Uterus-general	0.0357			
Breast hyperplasia	0.0890			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0213			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0167	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0123	0.1693	5.9051
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	
		Uterus_n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0038	0.0075	0.5104	1.9593
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0000	undef	0.0000
Lung	0.0000	0.0153	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency		% frequency
Development	0.0000	Breast	
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0042
		Uterus n	

Electronic Northern for SEQ. ID NO.: 33

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0663	0.0741	0.8942	1.1183
Small intestine	0.0640	0.0846	0.7561	1.3225
Ovary	0.1104	0.0165	6.6733	0.1499
Endocrine tissue	0.0958	0.1951	0.4912	2.0358
Gastrointestinal	0.0511	0.0426	1.1987	0.8343
Brain	0.1188	0.1527	0.7781	1.2851
Hematopoietic	0.0584	0.0863	0.6771	1.4769
Skin	0.1016	0.1136	0.8940	1.1186
Hepatic	0.0698	0.0000	undef	0.0000
Heart	0.0048	0.0776	0.0613	16.3199
Testicles	0.1304	0.0000	undef	0.0000
Lung	0.0230	0.0819	0.2811	3.5571
Stomach-esophagus	0.1620	0.1227	1.3209	0.7571
Muscle-skeleton	0.0580	0.1073	0.5402	1.8511
Kidney	0.1045	0.0480	2.1773	0.4593
Pancreas	0.0516	0.0959	0.5381	1.8583
Penis	0.0529	0.1491	0.3545	2.8205
Prostate	0.0749	0.0800	0.9360	1.0684
Uterus-endometrium	0.0632	0.0426	1.4843	0.6737
Uterus-myometrium	0.0676	0.0000	undef	0.0000
Uterus-general	0.1067	0.2309	0.4621	2.1640
Breast hyperplasia	0.1528	0.0000	undef	0.0000
Prostate hyperplasia	0.0480			
Seminal vesicle	0.0476			
Sensory organs	0.0534			
White blood cells	0.0235			
Cervix	0.1309			
	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency		% frequency
Development		Breast	
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0333	Ovary_t	0.1595
Hematopoietic	0.0626	Endocrine tissue	0.0152
Skin	0.0590	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0052
Heart-blood vessels	0.0260	Hematopoietic	0.0244
Lung	0.0391	Skin-muscle	0.0000
Suprarenal gland	0.0650	Testicles	0.0097
Kidney	0.0000	Lung	0.0000
Placenta	0.0432	Nerves	0.0573
Prostate	0.0424	Prostate	0.0181
Sensory organs	0.0249	Sensory Organs	0.0342
	0.0126	Sensory Organs	0.0000
		Uterus n	0.0333

Electronic Northern for SEQ. ID NO.: 34

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0038	0.0000	undef	0.0000
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0598	0.0501	19.9782
Endocrine tissue	0.0068	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0030	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0042	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0299	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0106			
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus n	

Electronic Northern for SEQ. ID NO.: 35

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000 undef	
Breast	0.0000	0.0038	0.0000 undef	
Small intestine	0.0061	0.0000	undef 0.0000	
Ovary	0.0030	0.0234	0.1279 7.8175	
Endocrine tissue	0.0000	0.0000	undef undef	
Gastrointestinal	0.0192	0.0185	1.0354 0.9658	
Brain	0.0015	0.0062	0.2400 4.1669	
Hematopoietic	0.0013	0.0000	undef 0.0000	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0000	0.0000	undef undef	
Testicles	0.0052	0.0061	0.8467 1.1810	
Lung	0.0000	0.0000	undef undef	
Stomach-esophagus	0.0000	0.0060	0.0000 undef	
Muscle-skeleton	0.0027	0.0000	undef 0.0000	
Kidney	0.0000	0.0110	0.0000 undef	
Pancreas	0.0000	0.0000	undef undef	
Penis	0.0000	0.0000	undef undef	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0000			
Uterus-general	0.0030			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0051
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 36

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0000	undef 0.0000	
Small intestine	0.0026	0.0000	undef 0.0000	
Ovary	0.0000	0.0000	undef undef	
Endocrine tissue	0.0000	0.0130	0.0000 undef	
Gastrointestinal	0.0000	0.0025	0.0000 undef	
Brain	0.0000	0.0139	0.0000 undef	
Hematopoietic	0.0022	0.0000	undef 0.0000	
Skin	0.0027	0.0000	undef 0.0000	
Hepatic	0.0073	0.0000	undef 0.0000	
Heart	0.0000	0.0000	undef undef	
Testicles	0.0000	0.0137	0.0000 undef	
Lung	0.0000	0.0234	0.0000 undef	
Stomach-esophagus	0.0021	0.0020	1.0161 0.9842	
Muscle-skeleton	0.0000	0.0153	0.0000 undef	
Kidney	0.0017	0.0000	undef 0.0000	
Pancreas	0.0027	0.0000	undef 0.0000	
Penis	0.0033	0.0000	undef 0.0000	
Prostate	0.0030	0.0267	0.1123 8.9035	
Uterus-endometrium	0.0000	0.0021	0.0000 undef	
Uterus-myometrium	0.0068	0.0000	undef 0.0000	
Uterus-general	0.0000	0.0000	undef undef	
Breast hyperplasia	0.0051	0.0000	undef 0.0000	
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0020
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 38

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef undef	
Small intestine	0.0000	0.0000	undef undef	
Ovary	0.0000	0.0000	undef undef	
Endocrine tissue	0.0000	0.0234	0.0000 undef	
Gastrointestinal	0.0000	0.0000	undef undef	
Brain	0.0000	0.0000	undef undef	
Hematopoietic	0.0000	0.0000	undef undef	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0000	0.0000	undef undef	
Testicles	0.0000	0.0000	undef undef	
Lung	0.0000	0.0000	undef undef	
Stomach-esophagus	0.3189	0.0153	20.7988	0.0481
Muscle-skeleton	0.0000	0.0000	undef undef	
Kidney	0.0000	0.0000	undef undef	
Pancreas	0.0000	0.0000	undef undef	
Penis	0.0000	0.0000	undef undef	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0000	0.0000	undef undef	
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 39

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0286	0.0000	undef
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0030	0.0072	0.4114	2.4307
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0021	0.0041	0.5080	1.9684
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0054	0.0137	0.3965	2.5219
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0021			
White blood cells	0.0043			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus n

Electronic Northern for SEQ. ID NO.: 40

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0077	0.5085	1.9666
Small intestine	0.0051	0.0056	0.9074	1.1021
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0208	0.1439	6.9489
Gastrointestinal	0.0102	0.0025	4.0755	0.2454
Brain	0.0115	0.0093	1.2425	0.8048
Hematopoietic	0.0044	0.0062	0.7200	1.3890
Skin	0.0053	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0021	0.0000	undef	0.0000
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0062	0.0061	1.0161	0.9842
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0120	0.1428	7.0040
Pancreas	0.0027	0.0068	0.3965	2.5219
Penis	0.0000	0.0000	undef	undef
Prostate	0.0030	0.0267	0.1123	8.9035
Uterus-endometrium	0.0065	0.0021	3.0709	0.3256
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0035			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0111	Ovary_t	0.0000
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0065
Lung	0.0071	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0164
Kidney	0.0247	Lung	0.0070
Placenta	0.0061	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0167
		Uterus_n	

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0208	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0096	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 42

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0037	0.0010	3.5998	0.2778
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0052	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0064	0.0000	undef	undef
Breast hyperplasia	0.0059	0.0000		
Prostate hyperplasia	0.0000	0.0000		
Seminal vesicle	0.0000	0.0000		
Sensory organs	0.0000	0.0000		
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

Electronic Northern for SEQ. ID NO.: 43

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0130	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0235			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0260	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000		undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 45

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0102	0.0000	undef
Breast	0.0090	0.0056	1.5879	0.6298
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0390	0.1535	6.5146
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0019	0.0231	0.0828	12.0723
Brain	0.0000	0.0031	0.0000	undef
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0037	0.0847	0.0433	23.0839
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0021	0.0102	0.2032	4.9209
Lung	0.0000	0.0077	0.0000	undef
Stomach-esophagus	0.0017	0.0000	undef	0.0000
Muscle-skeleton	0.0054	0.0000	undef	0.0000
Kidney	0.0000	0.0110	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0065	0.0000	undef	0.0000
Prostate	0.0135	0.0000	undef	0.0000
Prostate	0.0229	0.0068	3.3668	0.2970
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0096			
Uterus-general	0.0059			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0491
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0125

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0090	0.0263	0.3403	2.9389
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0170	0.0050	3.3962	0.2944
Gastrointestinal	0.0172	0.0046	3.7275	0.2683
Brain	0.0081	0.0216	0.3771	2.6517
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0117	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0083	0.0020	4.0643	0.2460
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0120	0.0060	1.9989	0.5003
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0017	0.0110	0.1496	6.6857
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0131	0.0021	6.1418	0.1628
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0043			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0171
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0000
Placenta	0.0121	Nerves	0.0137
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0117	0.0051	2.2882	0.4370
Breast	0.0090	0.0019	4.7637	0.2099
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0208	0.1439	6.9489
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0052	0.0041	1.2701	0.7873
Lung	0.0000	0.0077	0.0000	undef
Stomach-esophagus	0.0017	0.0180	0.0952	10.5060
Muscle-skeleton	0.0054	0.0000	undef	0.0000
Kidney	0.0083	0.0055	1.4957	0.6686
Pancreas	0.0090	0.0000	undef	0.0000
Penis	0.0000	0.0064	0.0000	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0064			
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0017			
White blood cells	0.0106			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0077
Sensory organs		Sensory Organs	0.0000
		Uterus n	

Electronic Northern for SEQ. ID NO.: 48

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0026	6.1018	0.1639
Breast	0.0179	0.0169	1.0586	0.9446
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0286	0.2093	4.7774
Endocrine tissue	0.0324	0.0251	1.2906	0.7749
Gastrointestinal	0.0287	0.0278	1.0354	0.9658
Brain	0.0229	0.0164	1.3949	0.7169
Hematopoietic	0.0107	0.0000	undef	0.0000
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0350	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0239	0.0225	1.0623	0.9414
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0120	0.0060	1.9989	0.5003
Kidney	0.0190	0.0137	1.3878	0.7206
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0210	0.0000	undef	0.0000
Prostate	0.0262	0.0085	3.0709	0.3256
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0068	3.3668	0.2970
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0356			
Sensory organs	0.0000			
White blood cells	0.0208			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0167	Ovary_n	0.1595
Brain	0.0188	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0320	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0162
Suprarenal gland	0.0254	Testicles	0.0077
Kidney	0.0124	Lung	0.0164
Placenta	0.0182	Nerves	0.0221
Prostate	0.0249	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0155
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 49

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0038	0.0056	0.6805	1.4694
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0057	0.0139	0.4142	2.4145
Brain	0.0037	0.0062	0.6000	1.6668
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0042	0.0275	0.1542	6.4853
Heart	0.0115	0.0000	undef	0.0000
Testicles	0.0021	0.0041	0.5080	1.9684
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0017	0.0000	undef	0.0000
Muscle-skeleton	0.0109	0.0137	0.7930	1.2610
Kidney	0.0066	0.0055	1.1966	0.8357
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0044	0.0064	0.6824	1.4654
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0068	0.0000	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0064			
Breast hyperplasia	0.0208			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0065
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0020
Placenta	Nerves 0.0205
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0042
	Uterus_n

Electronic Northern for SEQ. ID NO.: 50

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0179	0.4358	2.2944
Breast	0.0064	0.0094	0.6805	1.4694
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0052	0.0051	1.0079	0.9921
Hematopoietic	0.0080	0.0379	0.2117	4.7230
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0073	0.0102	0.7112	1.4060
Stomach-esophagus	0.0097	0.0153	0.6303	1.5866
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0027	0.0137	0.1983	5.0439
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0131	0.0064	2.0473	0.4885
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0272	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0235			
White blood cells	0.0043			
Cervix	0.0213			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus n

Electronic Northern for SEQ. ID NO.: 51

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0077	0.0000	undef
Breast	0.0026	0.0150	0.1701	5.8778
Small intestine	0.0061	0.0165	0.3707	2.6973
Ovary	0.0030	0.0208	0.1439	6.9489
Endocrine tissue	0.0119	0.0075	1.5849	0.6309
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0037	0.0072	0.5143	1.9446
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0074	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0062	0.0061	1.0161	0.9842
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0188	0.0060	3.1411	0.3184
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0153	0.0106	1.4331	0.6978
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0026			
Cervix	0.0106			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0136
Gastrointestinal 0.0000	Ovary_n 0.0000
Brain 0.0028	Ovary_t 0.0000
Hematopoietic 0.0000	Endocrine tissue 0.0000
Skin 0.0079	Fetal 0.0052
Hepatic 0.0000	Gastrointestinal 0.0122
Heart-blood vessels 0.0000	Hematopoietic 0.0456
Lung 0.0213	Skin-muscle 0.0065
Suprarenal gland 0.0072	Testicles 0.0077
Kidney 0.1014	Lung 0.0164
Placenta 0.0000	Nerves 0.0040
Prostate 0.0000	Prostate 0.0068
Sensory organs 0.0000	Sensory Organs 0.0000
	Uterus_n 0.0000

Electronic Northern for SEQ. ID NO.: 52

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0102	0.3814	2.6222
Breast	0.0179	0.0038	4.7637	0.2099
Small intestine	0.0092	0.0496	0.1854	5.3946
Ovary	0.0060	0.0260	0.2303	4.3431
Endocrine tissue	0.0153	0.0251	0.6113	1.6358
Gastrointestinal	0.0211	0.0463	0.4556	2.1950
Brain	0.0155	0.0103	1.5119	0.6614
Hematopoietic	0.0040	0.0758	0.0529	18.8919
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0388	0.0000	undef
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0177	0.0143	1.2338	0.8105
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0109	0.0274	0.3965	2.5219
Pancreas	0.0231	0.0221	1.0470	0.9551
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0204	0.3741	2.6732
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0256			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0095			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0278	Breast	0.0068
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0125	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0142	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0164
Placenta	0.0061	Nerves	0.0060
Prostate	0.0499	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0234	0.0153	1.5254	0.6555
Breast	0.0115	0.0113	1.0208	0.9796
Small intestine	0.0092	0.0165	0.5561	1.7982
Ovary	0.0090	0.0286	0.3140	3.1849
Endocrine tissue	0.0102	0.0125	0.8151	1.2268
Gastrointestinal	0.0230	0.0278	0.8283	1.2072
Brain	0.0148	0.0144	1.0285	0.9723
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0106	0.0275	0.3855	2.5941
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0125	0.0123	1.0161	0.9842
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0137	0.0120	1.1422	0.8755
Kidney	0.0136	0.0274	0.4956	2.0176
Pancreas	0.0099	0.0110	0.8974	1.1143
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0109	0.0192	0.5687	1.7585
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0087			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0052	0.0051	1.0079	0.9921
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0032	0.0000	undef	undef
Heart	0.0000	0.0000	undef	0.0000
Testicles	0.0031	0.0000	undef	undef
Lung	0.0097	0.0000	1.5241	0.6561
Stomach-esophagus	0.0017	0.0060	undef	0.0000
Muscle-skeleton	0.0000	0.0000	0.2856	3.5020
Kidney	0.0017	0.0221	undef	undef
Pancreas	0.0000	0.0000	0.0748	13.3713
Penis	0.0000	0.0043	undef	undef
Prostate	0.0000	0.0000	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0032	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency		% frequency
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0082
Hepatic	0.0260	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0164
Placenta	0.0121	Nerves	0.0060
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0083

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0204	0.1907	5.2444
Breast	0.0141	0.0150	0.9357	1.0687
Small intestine	0.0061	0.0496	0.1236	8.0920
Ovary	0.0120	0.0364	0.3289	3.0402
Endocrine tissue	0.0085	0.0050	1.6981	0.5889
Gastrointestinal	0.0096	0.0046	2.0708	0.4829
Brain	0.0140	0.0185	0.7600	1.3159
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0294	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0138	0.0412	0.3341	2.9932
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0156	0.0164	0.9526	1.0498
Stomach-esophagus	0.0193	0.0307	0.6303	1.5866
Muscle-skeleton	0.0103	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0017	0.0331	0.0499	20.0570
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0174	0.0234	0.7445	1.3433
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0136	1.6834	0.5940
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0238			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0139			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0222	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0304
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0260	Gastrointestinal	0.0488
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0072	Skin-muscle	0.0162
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0303	Nerves	0.0090
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus n	0.0250

Electronic Northern for SEQ. ID NO.: 56

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0153	0.5085	1.9666
Breast	0.0077	0.0132	0.5833	1.7144
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0234	0.1279	7.8175
Endocrine tissue	0.0085	0.0025	3.3962	0.2944
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0022	0.0072	0.3086	3.2409
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0201	0.0000	undef	0.0000
Testicles	0.0000	0.0468	0.0000	undef
Lung	0.0031	0.0102	0.3048	3.2806
Stomach-esophagus	0.0193	0.0153	1.2605	0.7933
Muscle-skeleton	0.0120	0.0120	0.9994	1.0006
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0276	0.0000	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0065	0.0085	0.7677	1.3026
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0182			
Cervix	0.0213			

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0152
Hematopoietic	0.0039	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0178	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0246
Placenta	0.0061	Nerves	0.0060
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 57

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0128	0.0150	0.8507	1.1756
Small intestine	0.0061	0.0165	0.3707	2.6973
Ovary	0.0030	0.0208	0.1439	6.9489
Endocrine tissue	0.0051	0.0226	0.2264	4.4166
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0074	0.0103	0.7200	1.3890
Hematopoietic	0.0174	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0085	0.0275	0.3084	3.2426
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0062	0.0102	0.6096	1.6403
Stomach-esophagus	0.0000	0.0307	0.0000	undef
Muscle-skeleton	0.0120	0.0060	1.9989	0.5003
Kidney	0.0217	0.0068	3.1722	0.3152
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0018	0.0000	undef	0.0000
Prostate	0.0044	0.0085	0.5118	1.9538
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0272	0.2806	3.5642
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0139			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0278	Breast	0.0068
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0188	Ovary_t	0.0051
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0076
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0142	Hematopoietic	0.0000
Lung	0.0145	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0124	Lung	0.0120
Placenta	0.0000	Nerves	0.0274
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0585	0.0332	1.7601	0.5681
Breast	0.0230	0.0132	1.7499	0.5715
Small intestine	0.0153	0.0827	0.1854	5.3946
Ovary	0.0150	0.0546	0.2741	3.6482
Endocrine tissue	0.0136	0.0150	0.9057	1.1042
Gastrointestinal	0.0192	0.0416	0.4602	2.1730
Brain	0.0163	0.0277	0.5866	1.7046
Hematopoietic	0.0374	0.0379	0.9881	1.0121
Skin	0.0404	0.0847	0.4765	2.0985
Hepatic	0.0143	0.0388	0.3676	2.7200
Heart	0.0297	0.0412	0.7196	1.3897
Testicles	0.0863	0.1169	0.7380	1.3551
Lung	0.0364	0.0266	1.3678	0.7311
Stomach-esophagus	0.0290	0.0767	0.3782	2.6444
Muscle-skeleton	0.0411	0.0360	1.1422	0.8755
Kidney	0.0190	0.0137	1.3878	0.7206
Pancreas	0.0132	0.0497	0.2659	3.7607
Penis	0.0359	0.0800	0.4493	2.2259
Prostate	0.0262	0.0128	2.0473	0.4885
Uterus-endometrium	0.0338	0.0528	0.6402	1.5621
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0089			
Sensory organs	0.0235			
White blood cells	0.0251			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0278	Breast	0.0000
Gastrointestinal	0.0528	Ovary_n	0.0000
Brain	0.1189	Ovary_t	0.0000
Hematopoietic	0.0275	Endocrine tissue	0.0093
Skin	0.0000	Fetal	0.0366
Hepatic	0.0520	Gastrointestinal	0.0057
Heart-blood vessels	0.0818	Hematopoietic	0.0389
Lung	0.0253	Skin-muscle	0.0154
Suprarenal gland	0.0254	Testicles	0.0491
Kidney	0.0371	Lung	0.0120
Placenta	0.0424	Nerves	0.0068
Prostate	0.0499	Prostate	0.0077
Sensory organs	0.0251	Sensory Organs	0.0250
		Uterus n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0038	0.0056	0.6805	1.4694
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0060	0.0390	0.1535	6.5146
Endocrine tissue	0.0102	0.0251	0.4075	2.4537
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0140	0.0082	1.7099	0.5848
Hematopoietic	0.0053	0.1515	0.0353	28.3379
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0104	0.0184	0.5645	1.7715
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0051	0.0180	0.2856	3.5020
Kidney	0.0109	0.0137	0.7930	1.2610
Pancreas	0.0099	0.0110	0.8974	1.1143
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0270	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0061			
Cervix	0.0213			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0835	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0375	Ovary_t	0.0203
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0213	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0162
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0246
Placenta	0.0182	Nerves	0.0241
Prostate	0.0249	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0230	0.0000	undef
Breast	0.0000	0.0150	0.0000	undef
Small intestine	0.0675	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0153	0.0139	1.1045	0.9054
Brain	0.0022	0.0154	0.1440	6.9448
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0323	0.0000	undef
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	6.3239	0.7179	8.8087	0.1135
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0089			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0106			
Sensory organs				
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.2721	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0354
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.2685
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0083
		Uterus n	

Electronic Northern for SEQ. ID NO.: 65

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0077	0.5085	1.9666
Breast	0.0064	0.0075	0.8507	1.1756
Small intestine	0.0245	0.0165	1.4830	0.6743
Ovary	0.0090	0.0520	0.1727	5.7908
Endocrine tissue	0.0085	0.0000	undef	0.0000
Gastrointestinal	0.0153	0.0324	0.4733	2.1127
Brain	0.0044	0.0123	0.3600	2.7779
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0381	0.0970	0.3922	2.5500
Heart	0.0074	0.0137	0.5397	1.8529
Testicles	0.0000	0.0000	undef	undef
Lung	0.0052	0.0082	0.6350	1.5747
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0086	0.0000	undef	0.0000
Kidney	0.0163	0.0616	0.2643	3.7829
Pancreas	0.0396	0.0055	7.1795	0.1393
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0000	0.0528	0.0000	undef
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0153	0.2863	0.0534	18.7357
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0089			
Sensory organs	0.0235			
White blood cells	0.0043			
Cervix	0.0319			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0222	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0122
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0228
Lung	0.0036	Skin-muscle	0.0162
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0082
Placenta	0.0242	Nerves	0.0010
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 67

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0102	0.3814	2.6222
Breast	0.0026	0.0169	0.1512	6.6125
Small intestine	0.0092	0.0165	0.5561	1.7982
Ovary	0.0060	0.0260	0.2303	4.3431
Endocrine tissue	0.0034	0.0075	0.4528	2.2083
Gastrointestinal	0.0057	0.0185	0.3106	3.2193
Brain	0.0044	0.0062	0.7200	1.3890
Hematopoietic	0.0094	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0031	0.0102	0.3048	3.2806
Stomach-esophagus	0.0097	0.0153	0.6303	1.5866
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0022	0.0085	0.2559	3.9077
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0235			
White blood cells	0.0061			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0272
Brain	0.0056	Ovary_t	0.0000
Hematopoietic	0.0188	Endocrine tissue	0.0000
Skin	0.0157		0.0245
Hepatic	0.0000	Fetal	0.0169
Heart-blood vessels	0.0000	Gastrointestinal	0.0000
Lung	0.0000	Hematopoietic	0.0171
Suprarenal gland	0.0036	Skin-muscle	0.0000
Kidney	0.0000	Testicles	0.0000
Placenta	0.0000	Lung	0.0328
Prostate	0.0121	Nerves	0.0080
Sensory organs	0.0000	Prostate	0.0000
	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0125

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0288	0.0000	undef	0.0000
Lung	0.0031	0.0000	undef	0.0000
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0102	0.0954	0.1067	9.3678
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0017			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0342
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0108	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0062	Nerves	0.0020
Prostate	0.0000	Nerves	0.0068
Sensory organs	0.0000	Prostate	0.0000
		Sensory Organs	0.0042
		Uterus n	

Electronic Northern for SEQ. ID NO.: 70

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0077	0.0094	0.8166	1.2245
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0060	0.0260	0.2303	4.3431
Endocrine tissue	0.0324	0.0075	4.3019	0.2325
Gastrointestinal	0.0134	0.0093	1.4496	0.6898
Brain	0.0111	0.0051	2.1599	0.4630
Hematopoietic	0.0040	0.0379	0.1059	9.4460
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0135	0.0102	1.3209	0.7571
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0109	0.0068	1.5861	0.6305
Pancreas	0.0099	0.0055	1.7949	0.5571
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0109	0.0085	1.2795	0.7815
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0130			
Cervix	0.0106			

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0118	Endocrine tissue	0.0101
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0041
Heart-blood vessels	0.0142	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0057
Suprarenal gland	0.0000	Testicles	0.0097
Kidney	0.0000	Lung	0.0154
Placenta	0.0182	Nerves	0.0164
Prostate	0.0249	Prostate	0.0070
Sensory organs	0.0126	Sensory Organs	0.0137
		Uterus_n	0.0000
			0.0083

Electronic Northern for SEQ. ID NO.: 72

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.1053	0.0895	1.1768	0.8498
Breast	0.0652	0.0846	0.7713	1.2966
Small intestine	0.1073	0.0992	1.0813	0.9248
Ovary	0.0629	0.1353	0.4649	2.1509
Endocrine tissue	0.0579	0.0451	1.2830	0.7794
Gastrointestinal	0.1379	0.2220	0.6213	1.6096
Brain	0.0702	0.0534	1.3153	0.7603
Hematopoietic	0.1056	0.1136	0.9293	1.0761
Skin	0.0587	0.0847	0.6931	1.4427
Hepatic	0.0285	0.1035	0.2757	3.6266
Heart	0.1293	0.0412	3.1353	0.3189
Testicles	0.0403	0.1754	0.2296	4.3556
Lung	0.0914	0.1063	0.8598	1.1631
Stomach-esophagus	0.0387	0.1840	0.2101	4.7599
Muscle-skeleton	0.0548	0.1260	0.4351	2.2982
Kidney	0.0814	0.1438	0.5665	1.7654
Pancreas	0.0363	0.1878	0.1936	5.1662
Penis	0.1138	0.0800	1.4227	0.7029
Prostate	0.0697	0.0958	0.7279	1.3738
Uterus-endometrium	0.1824	0.0000	undef	0.0000
Uterus-myometrium	0.0838	0.0951	0.8818	1.1341
Uterus-general	0.1171	0.0000	undef	0.0000
Breast hyperplasia	0.0671			
Prostate hyperplasia	0.0922			
Seminal vesicle	0.0712			
Sensory organs	0.0706			
White blood cells	0.1448			
Cervix	0.1810			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0340
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0253
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0163
Hepatic	Gastrointestinal 0.0122
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0292
Suprarenal gland	Testicles 0.0077
Kidney	Lung 0.0246
Placenta	Nerves 0.0090
Prostate	Prostate 0.0274
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0042

Electronic Northern for SEQ. ID NO.: 73

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0663	0.0895	0.7409	1.3497
Breast	0.0371	0.0489	0.7591	1.3174
Small intestine	0.0766	0.0000	undef	0.0000
Ovary	0.0270	0.0754	0.3573	2.7989
Endocrine tissue	0.0170	0.0326	0.5225	1.9139
Gastrointestinal	0.0805	0.0833	0.9664	1.0348
Brain	0.0177	0.0390	0.4547	2.1992
Hematopoietic	0.0896	0.0758	1.1822	0.8459
Skin	0.0551	0.1695	0.3249	3.0779
Hepatic	0.0238	0.0776	0.3064	3.2640
Heart	0.0604	0.1237	0.4883	2.0480
Testicles	0.0288	0.0702	0.4100	2.4391
Lung	0.0519	0.0429	1.2096	0.8267
Stomach-esophagus	0.0676	0.0843	0.8022	1.2466
Muscle-skeleton	0.0223	0.0240	0.9280	1.0775
Kidney	0.0353	0.0548	0.6443	1.5520
Pancreas	0.0132	0.0773	0.1709	5.8500
Penis	0.0838	0.0533	1.5724	0.6360
Prostate	0.0567	0.0255	2.2179	0.4509
Uterus-endometrium	0.0946	0.0000	undef	0.0000
Uterus-myometrium	0.0762	0.0679	1.1223	0.8911
Uterus-general	0.0407	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0505			
Seminal vesicle	0.0445			
Sensory organs	0.0235			
White blood cells	0.0772			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0272
Gastrointestinal	0.0305	Ovary_n	0.0000
Brain	0.0313	Ovary_t	0.1468
Hematopoietic	0.0393	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0105
Hepatic	0.0260	Gastrointestinal	0.0366
Heart-blood vessels	0.0285	Hematopoietic	0.0057
Lung	0.0145	Skin-muscle	0.0292
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0679	Lung	0.0328
Placenta	0.0364	Nerves	0.0040
Prostate	0.0997	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 74

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0234	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0468	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0110	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0353	0.0164	2.1591	0.4631
Lung	0.1836	0.1227	1.4969	0.6681
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0050	0.0221	0.2244	4.4571
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0128	0.1706	5.8615
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.1246	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix	0.0000	0.0000	undef	undef

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 76

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0077	0.0000	undef
Breast	0.0026	0.0301	0.0851	11.7556
Small intestine	0.0000	0.0331	0.0000	undef
Ovary	0.0030	0.0728	0.0411	24.3213
Endocrine tissue	0.0000	0.0100	0.0000	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0510	0.0596	0.8565	1.1675
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.1695	0.0217	46.1678
Hepatic	0.0523	0.1747	0.2996	3.3382
Heart	0.0138	0.0137	1.0023	0.9977
Testicles	0.0000	0.0935	0.0000	undef
Lung	0.0073	0.0818	0.0889	11.2478
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0240	0.2760	0.0869	11.5066
Kidney	0.3910	0.4108	0.9516	1.0508
Pancreas	0.1123	0.0387	2.9060	0.3441
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0068	0.2111	0.0320	31.2422
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.1908	0.0267	37.4714
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.1838			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0696	Breast	0.0000
Gastrointestinal	0.0194	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0128
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0164
Placenta	0.2302	Nerves	0.0231
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.1632	Sensory Organs	0.0310
		Uterus_n	0.0000

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0153	1.0170	0.9833
Breast	0.0090	0.0244	0.3664	2.7290
Small intestine	0.0123	0.0496	0.2472	4.0460
Ovary	0.0090	0.0338	0.2657	3.7640
Endocrine tissue	0.0136	0.0226	0.6038	1.6562
Gastrointestinal	0.0172	0.0324	0.5325	1.8779
Brain	0.0044	0.0216	0.2057	4.8614
Hematopoietic	0.0254	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0170	0.0137	1.2336	0.8107
Testicles	0.0000	0.0000	undef	undef
Lung	0.0073	0.0286	0.2540	3.9367
Stomach-esophagus	0.0000	0.0307	0.0000	undef
Muscle-skeleton	0.0051	0.0180	0.2856	3.5020
Kidney	0.0190	0.0068	2.7756	0.3603
Pancreas	0.0083	0.0110	0.7479	1.3371
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0131	0.0106	1.2284	0.8141
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0113			
Cervix	0.0213			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0250	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0152
Hematopoietic	0.0118	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0256
Hepatic	0.0260	Gastrointestinal	0.0122
Heart-blood vessels	0.0178	Hematopoietic	0.0000
Lung	0.0145	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0309
Kidney	0.0371	Lung	0.0164
Placenta	0.0061	Nerves	0.0100
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0377	Sensory Organs	0.1084
		Uterus n	0.0250

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0273	0.0332	0.8214	1.2174
Breast	0.0230	0.0188	1.2250	0.8164
Small intestine	0.0276	0.0331	0.8342	1.1988
Ovary	0.0210	0.0650	0.3224	3.1022
Endocrine tissue	0.0238	0.0276	0.8645	1.1567
Gastrointestinal	0.0172	0.0463	0.3728	2.6827
Brain	0.0118	0.0144	0.8228	1.2153
Hematopoietic	0.0214	0.0379	0.5646	1.7711
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0048	0.0259	0.1838	5.4400
Heart	0.0540	0.0550	0.9830	1.0173
Testicles	0.0173	0.0585	0.2952	3.3877
Lung	0.0322	0.0450	0.7159	1.3969
Stomach-esophagus	0.0290	0.0077	3.7816	0.2644
Muscle-skeleton	0.0240	0.0600	0.3998	2.5014
Kidney	0.0353	0.0548	0.6443	1.5520
Pancreas	0.0165	0.0221	0.7479	1.3371
Penis	0.0150	0.0267	0.5616	1.7807
Prostate	0.0240	0.0405	0.5926	1.6874
Uterus-endometrium	0.0270	0.1055	0.2561	3.9053
Uterus-myometrium	0.0381	0.0068	5.6113	0.1782
Uterus-general	0.0051	0.1908	0.0267	37.4714
Breast hyperplasia	0.0224			
Prostate hyperplasia	0.0297			
Seminal vesicle	0.0534			
Sensory organs	0.0588			
White blood cells	0.0234			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0557	Breast	0.0136
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0039	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0256
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0142	Hematopoietic	0.0000
Lung	0.0253	Skin-muscle	0.0583
Suprarenal gland	0.0507	Testicles	0.0231
Kidney	0.0432	Lung	0.0491
Placenta	0.0303	Nerves	0.0221
Prostate	0.1247	Prostate	0.0821
Sensory organs	0.0251	Sensory Organs	0.0000
		Uterus n	0.0416

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0026	0.0075	0.3403	2.9389
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0182	0.1645	6.0803
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0000	0.0139	0.0000	undef
Brain	0.0044	0.0041	1.0799	0.9260
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0033	0.0055	0.5983	1.6714
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0093
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0254	Skin-muscle	0.0000
Suprarenal gland	0.0062	Testicles	0.0309
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0060
Prostate	0.0126	Prostate	0.0068
Sensory organs		Sensory Organs	0.0000
		Uterus n	0.0000

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0128	0.3051	3.2777
Breast	0.0141	0.0150	0.9357	1.0687
Small intestine	0.0153	0.0000	undef	0.0000
Ovary	0.0090	0.0416	0.2159	4.6326
Endocrine tissue	0.0119	0.0176	0.6792	1.4722
Gastrointestinal	0.0096	0.0139	0.6903	1.4487
Brain	0.0126	0.0031	4.0798	0.2451
Hematopoietic	0.0080	0.1136	0.0706	14.1689
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0191	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0104	0.0164	0.6350	1.5747
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0069	0.0120	0.5711	1.7510
Kidney	0.0109	0.0137	0.7930	1.2610
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0131	0.0021	6.1418	0.1628
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0128	0.0000	undef	undef
Breast hyperplasia	0.0119			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0104			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	
	% frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.1595
Brain	Ovary_t	0.0152
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0070
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0057
Lung	Skin-muscle	0.0065
Suprarenal gland	Testicles	0.0231
Kidney	Lung	0.0082
Placenta	Nerves	0.0191
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.0155
	Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 82

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0351	0.0435	0.8076	1.2383
Breast	0.0576	0.0489	1.1778	0.8490
Small intestine	0.0337	0.0165	2.0391	0.4904
Ovary	0.0659	0.1353	0.4871	2.0531
Endocrine tissue	0.0801	0.0878	0.9121	1.0963
Gastrointestinal	0.0441	0.1203	0.3664	2.7294
Brain	0.1072	0.0298	3.5998	0.2778
Hematopoietic	0.0201	0.1515	0.1323	7.5568
Skin	0.0661	0.0000	undef	0.0000
Hepatic	0.0428	0.0582	0.7353	1.3600
Heart	0.0572	0.0687	0.8327	1.2010
Testicles	0.0460	0.1988	0.2315	4.3193
Lung	0.0416	0.0634	0.6555	1.5255
Stomach-esophagus	0.0290	0.0613	0.4727	2.1155
Muscle-skeleton	0.0360	0.0180	1.9989	0.5003
Kidney	0.0489	0.0411	1.1896	0.8406
Pancreas	0.1371	0.0552	2.4829	0.4028
Penis	0.0479	0.0000	undef	0.0000
Prostate	0.0741	0.0426	1.7402	0.5747
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0534	0.0475	1.1223	0.8911
Uterus-general	0.0407	0.0000	undef	0.0000
Breast hyperplasia	0.0639			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0623			
Sensory organs	0.0588			
White blood cells	0.0546			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0696	Breast	0.0068
Gastrointestinal	0.1971	Ovary_n	0.0000
Brain	0.0500	Ovary_t	0.0304
Hematopoietic	0.0551	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0262
Hepatic	0.1040	Gastrointestinal	0.1220
Heart-blood vessels	0.0427	Hematopoietic	0.0285
Lung	0.1120	Skin-muscle	0.0356
Suprarenal gland	0.1521	Testicles	0.0309
Kidney	0.0309	Lung	0.2211
Placenta	0.1212	Nerves	0.0502
Prostate	0.0748	Prostate	0.0615
Sensory organs	0.0628	Sensory Organs	0.1471
		Uterus_n	0.0125

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0077	2.0339	0.4917
Breast	0.0307	0.0169	1.8147	0.5510
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0120	0.0416	0.2878	3.4745
Endocrine tissue	0.0273	0.0176	1.5526	0.6441
Gastrointestinal	0.0153	0.0324	0.4733	2.1127
Brain	0.0192	0.0154	1.2479	0.8013
Hematopoietic	0.0147	0.0379	0.3882	2.5762
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0238	0.0065	3.6765	0.2720
Heart	0.0170	0.0137	1.2336	0.8107
Testicles	0.0230	0.0234	0.9839	1.0163
Lung	0.0177	0.0204	0.8637	1.1579
	0.0000	0.0153	0.0000	undef
Stomach-esophagus	0.0154	0.0060	2.5700	0.3891
Muscle-skeleton	0.0190	0.0000	undef	0.0000
Kidney	0.0132	0.0166	0.7977	1.2536
Pancreas	0.0240	0.0000	undef	0.0000
Penis	0.0109	0.0106	1.0236	0.9769
Prostate	0.0338	0.0000	undef	0.0000
Uterus-endometrium	0.0305	0.0000	undef	0.0000
Uterus-myometrium	0.0204	0.0000	undef	0.0000
Uterus-general	0.0416			
Breast hyperplasia	0.0208			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0235			
Sensory organs	0.0087			
White blood cells	0.0213			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0068
Gastrointestinal 0.0278	Ovary_n 0.1595
Brain 0.0056	Ovary_t 0.0051
Hematopoietic 0.0438	Endocrine tissue 0.0000
Skin 0.0039	Fetal 0.0111
Hepatic 0.0000	Gastrointestinal 0.0122
Heart-blood vessels 0.0000	Hematopoietic 0.0000
Lung 0.0427	Skin-muscle 0.0097
Suprarenal gland 0.0145	Testicles 0.0000
Kidney 0.0254	Lung 0.0491
Placenta 0.0062	Nerves 0.0231
Prostate 0.0000	Prostate 0.0342
Sensory organs 0.0000	Sensory Organs 0.0000
	Uterus n 0.0083

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0153	2.0339	0.4917
Breast	0.0192	0.0320	0.6005	1.6654
Small intestine	0.0245	0.0000	undef	0.0000
Ovary	0.0060	0.0416	0.1439	6.9489
Endocrine tissue	0.0273	0.0451	0.6038	1.6562
Gastrointestinal	0.0230	0.0093	2.4850	0.4024
Brain	0.0177	0.0164	1.0799	0.9260
Hematopoietic	0.0174	0.0379	0.4587	2.1798
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0381	0.0065	5.8824	0.1700
Heart	0.0159	0.0000	undef	0.0000
Testicles	0.0115	0.0351	0.3280	3.0489
Lung	0.0187	0.0123	1.5241	0.6561
Stomach-esophagus	0.0000	0.0460	0.0000	undef
Muscle-skeleton	0.0120	0.0000	undef	0.0000
Kidney	0.0109	0.0205	0.5287	1.8915
Pancreas	0.0083	0.0166	0.4986	2.0057
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0131	0.0064	2.0473	0.4885
Uterus-endometrium	0.0405	0.0528	0.7682	1.3018
Uterus-myometrium	0.0305	0.0204	1.4964	0.6683
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0327			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0165			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0272
Gastrointestinal 0.0557	Ovary_n 0.0000
Brain 0.0222	Ovary_t 0.0152
Hematopoietic 0.0250	Endocrine tissue 0.0000
Skin 0.0118	Fetal 0.0151
Hepatic 0.0000	Gastrointestinal 0.0000
Heart-blood vessels 0.0000	Hematopoietic 0.0259
Lung 0.0249	Skin-muscle 0.0000
Suprarenal gland 0.0181	Testicles 0.0246
Kidney 0.0000	Lung 0.0341
Placenta 0.0062	Nerves 0.0274
Prostate 0.0242	Prostate 0.0000
Sensory organs 0.0249	Sensory Organs 0.0125
	Uterus_n

Electronic Northern for SEQ. ID NO.: 85

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0102	0.0000 undef	
Breast	0.0051	0.0395	0.1296 7.7146	
Small intestine	0.0092	0.0165	0.5561 1.7982	
Ovary	0.0030	0.0312	0.0959 10.4234	
Endocrine tissue	0.0000	0.0050	0.0000 undef	
Gastrointestinal	0.0038	0.0139	0.2761 3.6217	
Brain	0.0081	0.0113	0.7200 1.3890	
Hematopoietic	0.0027	0.0000	undef 0.0000	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0074	0.0000	undef 0.0000	
Testicles	0.0000	0.0117	0.0000 undef	
Lung	0.0062	0.0020	3.0482 0.3281	
Stomach-esophagus	0.0097	0.0077	1.2605 0.7933	
Muscle-skeleton	0.0034	0.0120	0.2856 3.5020	
Kidney	0.0027	0.0000	undef 0.0000	
Pancreas	0.0033	0.0000	undef 0.0000	
Penis	0.0030	0.1066	0.0281 35.6140	
Prostate	0.0044	0.0043	1.0236 0.9769	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0076	0.0000	undef 0.0000	
Uterus-general	0.0153	0.0000	undef 0.0000	
Breast hyperplasia	0.0000	0.0030		
Prostate hyperplasia	0.0089	0.0000		
Seminal vesicle	0.0000	0.0026		
Sensory organs	0.0026	0.0106		
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0087
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0333

Electronic Northern for SEQ. ID NO.: 88

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0486	0.4014	2.4911
Breast	0.0064	0.0338	0.1890	5.2900
Small intestine	0.0153	0.0165	0.9268	1.0789
Ovary	0.0030	0.0182	0.1645	6.0803
Endocrine tissue	0.0136	0.0000	undef	0.0000
Gastrointestinal	0.0134	0.0139	0.9664	1.0348
Brain	0.0052	0.0123	0.4200	2.3811
Hematopoietic	0.0361	0.0379	0.9528	1.0496
Skin	0.0184	0.0847	0.2166	4.6168
Hepatic	0.0048	0.0388	0.1225	8.1599
Heart	0.0074	0.0962	0.0771	12.9706
Testicles	0.0115	0.0234	0.4920	2.0326
Lung	0.0665	0.0573	1.1612	0.8612
Stomach-esophagus	0.0193	0.0383	0.5042	1.9833
Muscle-skeleton	0.0788	0.0300	2.6271	0.3807
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0116	0.0166	0.6980	1.4326
Penis	0.0000	0.0800	0.0000	undef
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0954	0.0000	undef
Uterus-general	0.0128			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.1682			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0557
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0064
Hepatic	Gastrointestinal 0.0122
Heart-blood vessels	Hematopoietic 0.0057
Lung	Skin-muscle 0.0032
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0125
	Uterus_n

Electronic Northern for SEQ. ID NO.: 89

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0128	0.3051	3.2777
Breast	0.0153	0.0038	4.0832	0.2449
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0068	0.0025	2.7170	0.3681
Gastrointestinal	0.0077	0.0046	1.6567	0.6036
Brain	0.0052	0.0021	2.5199	0.3968
Hematopoietic	0.0174	0.0000	undef	0.0000
Skin	0.0844	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0201	0.0275	0.7324	1.3653
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0156	0.0061	2.5402	0.3937
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0329	0.1066	0.3089	3.2376
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0121			
Cervix	0.0852			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development		Breast 0.0136
Gastrointestinal	0.0139	Ovary_n 0.0000
Brain	0.0028	Ovary_t 0.0000
Hematopoietic	0.0063	Endocrine tissue 0.0000
Skin	0.0079	Fetal 0.0087
Hepatic	0.0000	Gastrointestinal 0.0244
Heart-blood vessels	0.0000	Hematopoietic 0.0000
Lung	0.0107	Skin-muscle 0.0154
Suprarenal gland	0.0000	Testicles 0.0164
Kidney	0.0000	Lung 0.0020
Placenta	0.0061	Nerves 0.0000
Prostate	0.0000	Prostate 0.0000
Sensory organs	0.0000	Sensory Organs 0.0125
		Uterus_n

Electronic Northern for SEQ. ID NO.: 90

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0038	0.0169	0.2268	4.4083
Small intestine	0.0184	0.0165	1.1122	0.8991
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0051	0.0326	0.1567	6.3796
Gastrointestinal	0.0057	0.0093	0.6213	1.6096
Brain	0.0067	0.0062	1.0799	0.9260
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0201	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0083	0.0143	0.5806	1.7223
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0109	0.0137	0.7930	1.2610
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0065	0.0128	0.5118	1.9538
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0356			
Sensory organs	0.0118			
White blood cells	0.0052			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0064
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0057
Lung	Skin-muscle 0.0130
Suprarenal gland	Testicles 0.0231
Kidney	Lung 0.0164
Placenta	Nerves 0.0060
Prostate	Prostate 0.0137
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0042

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0077	1.0170	0.9833
Breast	0.0051	0.0094	0.5444	1.8368
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0119	0.0150	0.7925	1.2619
Gastrointestinal	0.0057	0.0093	0.6213	1.6096
Brain	0.0081	0.0082	0.9899	1.0102
Hematopoietic	0.0120	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0127	0.0412	0.3084	3.2426
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0073	0.0307	0.2371	4.2179
Stomach-esophagus	0.0290	0.0383	0.7563	1.3222
Muscle-skeleton	0.0086	0.0060	1.4278	0.7004
Kidney	0.0054	0.0274	0.1983	5.0439
Pancreas	0.0033	0.0166	0.1994	5.0142
Penis	0.0150	0.0533	0.2808	3.5614
Prostate	0.0000	0.0106	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0035			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0071	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0328
Placenta	0.0121	Nerves	0.0040
Prostate	0.0000	Nerves	0.0274
Sensory organs	0.0000	Prostate	0.0000
		Sensory Organs	0.0083
		Uterus n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef undef	
Breast	0.0038	0.0132	0.2917 3.4287	
Small intestine	0.0031	0.0165	0.1854 5.3946	
Ovary	0.0000	0.0182	0.0000 undef	
Endocrine tissue	0.0051	0.0075	0.6792 1.4722	
Gastrointestinal	0.0038	0.0000	undef 0.0000	
Brain	0.0015	0.0000	undef 0.0000	
Hematopoietic	0.0000	0.0000	undef undef	
Skin	0.0073	0.0000	undef 0.0000	
Hepatic	0.0048	0.0000	undef 0.0000	
Heart	0.0011	0.0137	0.0771 12.9706	
Testicles	0.0000	0.0000	undef undef	
Lung	0.0145	0.0061	2.3708 0.4218	
Stomach-esophagus	0.0000	0.0153	0.0000 undef	
Muscle-skeleton	0.0017	0.0000	undef 0.0000	
Kidney	0.0054	0.0000	undef 0.0000	
Pancreas	0.0017	0.0000	undef 0.0000	
Penis	0.0030	0.0000	undef 0.0000	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0051	0.0000	undef 0.0000	
Uterus-general	0.0032			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0235			
Sensory organs	0.0139			
White blood cells	0.0106			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development		Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0164
Placenta	0.0061	Nerves	0.0040
Prostate	0.0000	Nerves	0.0000
Sensory organs	0.0000	Prostate	0.0000
		Sensory Organs	0.0000
		Uterus n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0153	0.0000	undef
Small intestine	0.0077	0.0113	0.6805	1.4694
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0286	0.1047	9.5548
Gastrointestinal	0.0034	0.0075	0.4528	2.2083
Brain	0.0019	0.0093	0.2071	4.8289
Hematopoietic	0.0059	0.0082	0.7200	1.3890
Skin	0.0067	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0042	0.0000	undef	0.0000
Lung	0.0115	0.0234	0.4920	2.0326
Stomach-esophagus	0.0021	0.0061	0.3387	2.9526
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0051	0.0000	undef	0.0000
Pancreas	0.0054	0.0068	0.7930	1.2610
Penis	0.0017	0.0331	0.0499	20.0570
Prostate	0.0090	0.0267	0.3369	2.9678
Uterus-endometrium	0.0044	0.0021	2.0473	0.4885
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032	0.0000	undef	0.0000
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency		% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0063	Endocrine tissue	0.0245
Skin	0.0039	Fetal	0.0116
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0062	Nerves	0.0070
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0115	0.0132	0.8750	1.1429
Small intestine	0.0337	0.0496	0.6797	1.4713
Ovary	0.0030	0.0390	0.0768	13.0292
Endocrine tissue	0.0085	0.0251	0.3396	2.9444
Gastrointestinal	0.0747	0.0879	0.8501	1.1763
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0351	0.0000	undef
Lung	0.0042	0.0143	0.2903	3.4446
Lung	0.0483	0.0077	6.3027	0.1587
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0163	0.0137	1.1896	0.8406
Kidney	0.0231	0.0166	1.3960	0.7163
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0065	0.0106	0.6142	1.6282
Prostate	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0064			
Uterus-general	0.0119			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0106			
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0083	Ovary_t	0.0000
Hematopoietic	0.0188	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0035
Heart-blood vessels	0.0036	Hematopoietic	0.0244
Lung	0.0108	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0246
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0000

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.1092	0.0460	2.3729	0.4214
Breast	0.0627	0.0865	0.7249	1.3795
Small intestine	0.1012	0.1158	0.8739	1.1443
Ovary	0.0599	0.1509	0.3970	2.5190
Endocrine tissue	0.0852	0.2984	0.2854	3.5039
Gastrointestinal	0.0900	0.0925	0.9733	1.0274
Brain	0.1811	0.0637	2.8450	0.3515
Hematopoietic	0.0521	0.1136	0.4587	2.1798
Skin	0.0587	0.0000	undef	0.0000
Hepatic	0.0809	0.0582	1.3889	0.7200
Heart	0.1092	0.0962	1.1344	0.8815
Testicles	0.0230	0.0234	0.9839	1.0163
Lung	0.0634	0.1104	0.5739	1.7425
Stomach-esophagus	0.0387	0.0460	0.8404	1.1900
Muscle-skeleton	0.0463	0.0420	1.1014	0.9079
Kidney	0.0706	0.1369	0.5155	1.9400
Pancreas	0.0743	0.1049	0.7085	1.4114
Penis	0.1467	0.0800	1.8345	0.5451
Prostate	0.0567	0.0873	0.6491	1.5405
Uterus-endometrium	0.0811	0.0000	undef	0.0000
Uterus-myometrium	0.1067	0.1155	0.9242	1.0820
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.1407			
Prostate hyperplasia	0.0713			
Seminal vesicle	0.0534			
Sensory organs	0.0353			
White blood cells	0.0390			
Cervix	0.0532			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0068
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0253
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0116
Hepatic	Gastrointestinal 0.0122
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0454
Suprarenal gland	Testicles 0.0077
Kidney	Lung 0.0246
Placenta	Nerves 0.0753
Prostate	Prostate 0.0205
Sensory organs	Sensory Organs 0.0077
	Uterus_n 0.0500

Electronic Northern for SEQ. ID NO.: 96

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0057	0.0093	0.6213	1.6096
Brain	0.0015	0.0041	0.3600	2.7779
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0061	0.1693	5.9051
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0135	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0136	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0030			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0017			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 97

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0077	0.0075	1.0208	0.9796
Small intestine	0.0061	0.0331	0.1854	5.3946
Ovary	0.0030	0.0390	0.0768	13.0292
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0044	0.0154	0.2880	3.4724
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0095	0.0970	0.0980	10.1999
Heart	0.0000	0.0000	undef	undef
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0789	0.0532	1.4850	0.6734
Stomach-esophagus	0.0290	0.0077	3.7816	0.2644
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0205	0.1322	7.5658
Pancreas	0.0033	0.0055	0.5983	1.6714
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0153	0.0021	7.1654	0.1396
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0445			
Sensory organs	0.1411			
White blood cells	0.0026			
Cervix	0.1917			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0340
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0013	0.0056	0.2268	4.4083
Ovary	0.0092	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0130	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0093	0.0000	undef
Hematopoietic	0.0007	0.0021	0.3600	2.7779
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0011	0.0000	undef	0.0000
Lung	0.0000	0.0234	0.0000	undef
Stomach-esophagus	0.0021	0.0020	1.0161	0.9842
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0735
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus n	

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0026	1.5254	0.6555
Small intestine	0.0090	0.0056	1.5879	0.6298
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0156	0.0000	undef
Gastrointestinal	0.0051	0.0025	2.0377	0.4907
Brain	0.0019	0.0046	0.4142	2.4145
Hematopoietic	0.0015	0.0041	0.3600	2.7779
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0074	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0031	0.0000	undef	0.0000
Muscle-skeleton	0.0097	0.0000	undef	0.0000
Kidney	0.0103	0.0060	1.7133	0.5837
Pancreas	0.0081	0.0068	1.1896	0.8406
Penis	0.0050	0.0000	undef	0.0000
Prostate	0.0090	0.0000	undef	0.0000
Uterus-endometrium	0.0044	0.0064	0.6824	1.4654
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0204
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0101
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0134
Heart-blood vessels	0.0000	Hematopoietic	0.0122
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0097
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0164
Prostate	0.0424	Prostate	0.0100
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0077
			0.0042

Electronic Northern for SEQ. ID NO.: 100

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0179	1.7434	0.5736
Breast	0.0205	0.0244	0.8376	1.1939
Small intestine	0.0675	0.0000	undef	0.0000
Ovary	0.0060	0.0442	0.1354	7.3832
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0862	0.0463	1.8638	0.5365
Brain	0.0067	0.0133	0.4984	2.0063
Hematopoietic	0.0120	0.0000	undef	0.0000
Skin	0.0477	0.0000	undef	0.0000
Hepatic	0.0143	0.0388	0.3676	2.7200
Heart	0.0212	0.0412	0.5140	1.9456
Testicles	0.0230	0.0234	0.9839	1.0163
Lung	0.0374	0.0450	0.8313	1.2029
Stomach-esophagus	0.0290	0.0000	undef	0.0000
Muscle-skeleton	0.0137	0.0600	0.2284	4.3775
Kidney	0.0054	0.0274	0.1983	5.0439
Pancreas	0.0066	0.0442	0.1496	6.6857
Penis	0.0449	0.0267	1.6847	0.5936
Prostate	0.0240	0.0234	1.0236	0.9769
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0136	1.6834	0.5940
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0384			
Prostate hyperplasia	0.0238			
Seminal vesicle	0.0534			
Sensory organs	0.0235			
White blood cells	0.0303			
Cervix	0.0319			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0304
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0064
Heart-blood vessels	0.0000	Hematopoietic	0.0122
Lung	0.0213	Skin-muscle	0.0000
Suprarenal gland	0.0072	Testicles	0.0227
Kidney	0.0000	Lung	0.0309
Placenta	0.0000	Nerves	0.0164
Prostate	0.0182	Prostate	0.0020
Sensory organs	0.0000	Sensory Organs	0.0137
		Uterus_n	0.0000
			0.0042

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0077	0.5085	1.9666
Small intestine	0.0000	0.0188	0.0000	undef
Ovary	0.0245	0.0000	undef	0.0000
Endocrine tissue	0.0120	0.0442	0.2709	3.6916
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0134	0.0185	0.7248	1.3797
Hematopoietic	0.0007	0.0072	0.1029	9.7228
Skin	0.0321	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0129	0.0000	undef
Testicles	0.0021	0.0000	undef	0.0000
Lung	0.0000	0.0234	0.0000	undef
Stomach-esophagus	0.0478	0.0450	1.0623	0.9414
Muscle-skeleton	0.0676	0.0690	0.9804	1.0200
Kidney	0.0069	0.0000	undef	0.0000
Pancreas	0.0000	0.0068	0.0000	undef
Penis	0.0116	0.0055	2.0940	0.4775
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0065	0.0128	0.5118	1.9538
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.1101			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0139	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0366
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0234	0.0588	0.3979	2.5129
Breast	0.0179	0.0507	0.3529	2.8339
Small intestine	0.0245	0.0000	undef	0.0000
Ovary	0.0180	0.0546	0.3289	3.0402
Endocrine tissue	0.0324	0.0251	1.2906	0.7749
Gastrointestinal	0.0364	0.0786	0.4629	2.1603
Brain	0.0067	0.0216	0.3086	3.2409
Hematopoietic	0.0174	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0323	0.1471	6.7999
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0270	0.0225	1.2008	0.8328
Stomach-esophagus	0.0290	0.0383	0.7563	1.3222
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0326	0.0616	0.5287	1.8915
Pancreas	0.0132	0.0607	0.2176	4.5964
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0458	0.0617	0.7412	1.3491
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0352			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0356			
Sensory organs	0.0353			
White blood cells	0.0069			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency		% frequency
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0136
Brain	0.0167	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0253
Skin	0.0079	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0169
Heart-blood vessels	0.0000	Hematopoietic	0.0488
Lung	0.0325	Skin-muscle	0.0114
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0231
Placenta	0.0303	Nerves	0.0164
Prostate	0.0249	Prostate	0.0100
Sensory organs	0.0000	Sensory Organs	0.0205
		Uterus n	0.0077
			0.0083

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0351	0.0256	1.3729	0.7284
Small intestine	0.0077	0.0094	0.8166	1.2245
Ovary	0.0153	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0156	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0211	0.0463	0.4556	2.1950
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0110	0.0000	undef	0.0000
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0125	0.0204	0.6096	1.6403
Stomach-esophagus	0.0290	0.0307	0.9454	1.0578
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0244	0.0068	3.5687	0.2802
Pancreas	0.0066	0.0110	0.5983	1.6714
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0109	0.0170	0.6398	1.5631
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0954	0.0000	undef
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0178			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0272
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0010
Placenta	0.0242	Nerves	0.0137
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	

Electronic Northern for SEQ. ID NO.: 105

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0230	1.3559	0.7375
Breast	0.0435	0.0320	1.3611	0.7347
Small intestine	0.0429	0.0165	2.5952	0.3853
Ovary	0.0210	0.0676	0.3100	3.2263
Endocrine tissue	0.0341	0.0752	0.4528	2.2083
Gastrointestinal	0.0230	0.0185	1.2425	0.8048
Brain	0.0525	0.0554	0.9466	1.0564
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0330	0.0000	undef	0.0000
Hepatic	0.0143	0.0259	0.5515	1.8133
Heart	0.0329	0.0962	0.3414	2.9288
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0166	0.0327	0.5080	1.9684
Stomach-esophagus	0.0193	0.0307	0.6303	1.5866
Muscle-skeleton	0.0343	0.0240	1.4278	0.7004
Kidney	0.0624	0.0822	0.7600	1.3158
Pancreas	0.0182	0.0055	3.2906	0.3039
Penis	0.0419	0.0000	undef	0.0000
Prostate	0.0174	0.0405	0.4310	2.3202
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0381	0.0136	2.8057	0.3564
Uterus-general	0.0662	0.0954	0.6939	1.4412
Breast hyperplasia	0.0608			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0623			
Sensory organs	0.0235			
White blood cells	0.0035			
Cervix	0.0213			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0500	Ovary_t	0.0101
Hematopoietic	0.0876	Endocrine tissue	0.0490
Skin	0.0039	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0488
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0142	Skin-muscle	0.0356
Suprarenal gland	0.0434	Testicles	0.0154
Kidney	0.0000	Lung	0.0410
Placenta	0.0556	Nerves	0.0402
Prostate	0.0364	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
	0.1130	Uterus_n	0.0375

Electronic Northern for SEQ. ID NO.: 106

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0639	0.3051	3.2777
Breast	0.0333	0.0470	0.7077	1.4129
Small intestine	0.0399	0.1819	0.2191	4.5647
Ovary	0.0150	0.0702	0.2132	4.6905
Endocrine tissue	0.0238	0.0903	0.2642	3.7857
Gastrointestinal	0.0900	0.1110	0.8111	1.2329
Brain	0.0067	0.0267	0.2492	4.0126
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0587	0.0000	undef	0.0000
Hepatic	0.0143	0.0323	0.4412	2.2666
Heart	0.0011	0.0962	0.0110	90.7941
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0062	0.0184	0.3387	2.9526
Stomach-esophagus	0.0483	0.3527	0.1370	7.2985
Muscle-skeleton	0.0000	0.0360	0.0000	undef
Kidney	0.0733	0.1575	0.4655	2.1483
Pancreas	0.0694	0.0276	2.5128	0.3980
Penis	0.0090	0.0533	0.1685	5.9357
Prostate	0.0109	0.0255	0.4265	2.3446
Uterus-endometrium	0.0270	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0272	0.2806	3.5642
Uterus-general	0.0000	0.4771	0.0000	undef
Breast hyperplasia	0.0576			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.1068			
Sensory organs	0.0235			
White blood cells	0.0061			
Cervix	0.0319			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0136
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0111	Ovary_t	0.0101
Hematopoietic	0.0813	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0122
Hepatic	0.0000	Gastrointestinal	0.4149
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0145	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0309	Lung	0.0573
Placenta	0.0121	Nerves	0.0040
Prostate	0.0249	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 107

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0078	0.0204	0.3814	2.6222
Small intestine	0.0102	0.0132	0.7777	1.2858
Ovary	0.0153	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0208	0.0000	undef
Gastrointestinal	0.0119	0.0075	1.5849	0.6309
Brain	0.0307	0.0093	3.3134	0.3018
Hematopoietic	0.0111	0.0144	0.7714	1.2964
Skin	0.0094	0.0379	0.2470	4.0483
Hepatic	0.0441	0.0000	undef	0.0000
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0170	0.0000	undef	0.0000
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0229	0.0245	0.9314	1.0737
Muscle-skeleton	0.0097	0.0000	undef	0.0000
Kidney	0.0034	0.0120	0.2856	3.5020
Pancreas	0.0190	0.0205	0.9252	1.0808
Penis	0.0083	0.0110	0.7479	1.3371
Prostate	0.0030	0.0267	0.1123	8.9035
Uterus-endometrium	0.0065	0.0106	0.6142	1.6282
Uterus-myometrium	0.0405	0.0000	undef	0.0000
Uterus-general	0.0000	0.0272	0.0000	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0096			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0191			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	
Gastrointestinal	0.0278	Ovary_n	0.0068
Brain	0.0083	Ovary_t	0.0000
Hematopoietic	0.0188	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0041
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0107	Skin-muscle	0.0097
Suprarenal gland	0.0072	Testicles	0.0000
Kidney	0.0254	Lung	0.0082
Placenta	0.0185	Nerves	0.0131
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0125

Electronic Northern for SEQ. ID NO.: 110

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0078	0.0102	0.7627	1.3111
Small intestine	0.0166	0.0262	0.5898	1.6955
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0060	0.0390	0.1535	6.5146
Gastrointestinal	0.0392	0.0527	0.7439	1.3442
Brain	0.0153	0.0370	0.4142	2.4145
Hematopoietic	0.0059	0.0072	0.8228	1.2153
Skin	0.0080	0.0000	undef	0.0000
Hepatic	0.0110	0.0000	undef	0.0000
Heart	0.0000	0.0129	0.0000	undef
Testicles	0.0064	0.0687	0.0925	10.8088
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0239	0.0470	0.5080	1.9684
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0120	0.0120	0.9994	1.0006
Pancreas	0.0299	0.0000	undef	0.0000
Penis	0.0182	0.0110	1.6453	0.6078
Prostate	0.0210	0.0000	undef	0.0000
Uterus-endometrium	0.0305	0.0106	2.8662	0.3489
Uterus-myometrium	0.0203	0.1055	0.1920	5.2070
Uterus-general	0.0076	0.0136	0.5611	1.7821
Breast hyperplasia	0.0102	0.0000	undef	0.0000
Prostate hyperplasia	0.0352			
Seminal vesicle	0.0446			
Sensory organs	0.0267			
White blood cells	0.0353			
Cervix	0.0147			
	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal		Ovary_n	0.0068
Brain	0.0000	Ovary_t	0.1595
Hematopoietic	0.0222	Endocrine tissue	0.0101
Skin	0.0000	Fetal	0.0000
Hepatic	0.0197	Gastrointestinal	0.0408
Heart-blood vessels	0.0000	Hematopoietic	0.0366
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0178	Testicles	0.0259
Kidney	0.0145	Lung	0.0000
Placenta	0.0000	Nerves	0.0410
Prostate	0.0185	Prostate	0.0151
Sensory organs	0.0000	Sensory Organs	0.0342
	0.0000	Uterus_n	0.0155
	0.0126		0.0125

Electronic Northern for SEQ. ID NO.: 111

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0117	0.0460	0.2542	3.9333
Small intestine	0.0192	0.0376	0.5104	1.9593
Ovary	0.0000	0.0496	0.0000	undef
Endocrine tissue	0.0030	0.0234	0.1279	7.8175
Gastrointestinal	0.0017	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0007	0.0000	undef	0.0000
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0147	0.0000	undef	0.0000
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0062	0.0102	0.6096	1.6403
Muscle-skeleton	0.0193	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0271	0.0137	1.9826	0.5044
Penis	0.0132	0.0221	0.5983	1.6714
Prostate	0.0030	0.0267	0.1123	8.9035
Uterus-endometrium	0.0240	0.0298	0.8043	1.2434
Uterus-myometrium	0.0000	0.0528	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0352	0.0954	0.0000	undef
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development		Breast
Gastrointestinal	0.0000	Ovary_n
Brain	0.0000	Ovary_t
Hematopoietic	0.0000	Endocrine tissue
Skin	0.0000	Fetal
Hepatic	0.0000	Gastrointestinal
Heart-blood vessels	0.0000	Hematopoietic
Lung	0.0000	Skin-muscle
Suprarenal gland	0.0000	Testicles
Kidney	0.0000	Lung
Placenta	0.0000	Nerves
Prostate	0.0000	Prostate
Sensory organs	0.0000	Sensory Organs
		Uterus_n

Electronic Northern for SEQ. ID NO.: 112

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0051	0.0207	0.2475	4.0410
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0030	0.0338	0.0886	11.2920
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0038	0.0185	0.2071	4.8289
Brain	0.0022	0.0092	0.2400	4.1669
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0037	0.0847	0.0433	23.0839
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0053	0.0275	0.1927	5.1882
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0042	0.0041	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0109	0.0000	undef	0.0000
Kidney	0.0033	0.0055	0.5983	1.6714
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0044	0.0000	undef	0.0000
Prostate	0.0135	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0000			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0118			
Sensory organs	0.0009			
White blood cells	0.0213			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0354
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0071	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0062	Nerves	0.0000
Prostate	0.0000	Prostate	0.0155
Sensory organs	0.0249	Sensory Organs	0.0375
	0.0251	Uterus_n	

Electronic Northern for SEQ. ID NO.: 113

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0409	0.2860	3.4963
Breast	0.0256	0.0376	0.6805	1.4694
Small intestine	0.0399	0.0000	undef	0.0000
Ovary	0.0090	0.0390	0.2303	4.3431
Endocrine tissue	0.0477	0.0702	0.6792	1.4722
Gastrointestinal	0.0479	0.0231	2.0708	0.4829
Brain	0.0229	0.0349	0.6564	1.5234
Hematopoietic	0.0281	0.0000	undef	0.0000
Skin	0.0624	0.0000	undef	0.0000
Hepatic	0.0048	0.0259	0.1838	5.4400
Heart	0.0519	0.0000	undef	0.0000
Testicles	0.0230	0.0468	0.4920	2.0326
Lung	0.0270	0.0491	0.5504	1.8170
Stomach-esophagus	0.0387	0.0230	1.6807	0.5950
Muscle-skeleton	0.0377	0.0840	0.4487	2.2286
Kidney	0.0462	0.0411	1.1235	0.8901
Pancreas	0.0116	0.0276	0.4188	2.3877
Penis	0.0150	0.0533	0.2808	3.5614
Prostate	0.0283	0.0490	0.5786	1.7284
Uterus-endometrium	0.0541	0.0528	1.0243	0.9763
Uterus-myometrium	0.0305	0.0272	1.1223	0.8911
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0386			
Seminal vesicle	0.0267			
Sensory organs	0.0353			
White blood cells	0.0312			
Cervix	0.0213			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0611	Ovary_n	0.1595
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0157	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0320	Hematopoietic	0.0000
Lung	0.0397	Skin-muscle	0.0000
Suprarenal gland	0.0507	Testicles	0.0164
Kidney	0.0247	Lung	0.0050
Placenta	0.0303	Nerves	0.0068
Prostate	0.1247	Prostate	0.0000
Sensory organs	0.0377	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 115

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0702	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0192	0.0185	1.0354	0.9658
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0058	0.0000	undef	0.0000
Testicles	0.0052	0.0020	2.5402	0.3937
Lung	0.0193	0.0230	0.8404	1.1900
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0110	0.1496	6.6857
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0065	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0954	0.0000	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0167
		Uterus_n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0128	0.6102	1.6389
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0517	0.0879	0.5886	1.6991
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0381	0.0518	0.7353	1.3600
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0164	0.0635	15.7470
Lung	0.0290	0.0230	1.2605	0.7933
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0033	0.0110	0.2991	3.3428
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0022	0.0043	0.5118	1.9538
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0051	0.0000	undef	0.0000
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0051
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus n	0.0000

Electronic Northern for SEQ. ID NO.: 120

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000 undef	
Breast	0.0013	0.0056	0.2268 4.4083	
Small intestine	0.0031	0.0000	undef 0.0000	
Ovary	0.0000	0.0156	0.0000 undef	
Endocrine tissue	0.0000	0.0000	undef undef	
Gastrointestinal	0.0019	0.0046	0.4142 2.4145	
Brain	0.0022	0.0031	0.7200 1.3890	
Hematopoietic	0.0040	0.0000	undef 0.0000	
Skin	0.0073	0.0000	undef 0.0000	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0042	0.0000	undef 0.0000	
Testicles	0.0058	0.0000	undef 0.0000	
Lung	0.0010	0.0061	0.1693 5.9051	
Stomach-esophagus	0.0097	0.0000	undef 0.0000	
Muscle-skeleton	0.0017	0.0000	undef 0.0000	
Kidney	0.0027	0.0068	0.3965 2.5219	
Pancreas	0.0000	0.0000	undef undef	
Penis	0.0030	0.0000	undef 0.0000	
Prostate	0.0022	0.0021	1.0236 0.9769	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0000	0.0068	0.0000 undef	
Uterus-general	0.0051	0.0000	undef 0.0000	
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0043			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0260	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0082
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0249	Prostate	0.0155
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 121

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0153	0.7627	1.3111
Breast	0.0026	0.0132	0.1944	5.1431
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0030	0.0062	0.4800	2.0835
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.1760	0.0518	3.4008	0.2941
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0010	0.0082	0.1270	7.8735
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0188	0.0060	3.1411	0.3184
Kidney	0.0081	0.0000	undef	0.0000
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0174	0.0277	0.6299	1.5875
Uterus-endometrium	0.0000	0.0528	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032	0.0954	0.0000	undef
Breast hyperplasia	0.0119			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0235			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0203
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0035
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0010
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0000

Electronic Northern for SEQ. ID NO.: 122

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.1053	0.1125	0.9361	1.0683
Breast	0.1164	0.1015	1.1468	0.8720
Small intestine	0.0491	0.0662	0.7415	1.3487
Ovary	0.0479	0.1015	0.4723	2.1173
Endocrine tissue	0.0562	0.0251	2.2415	0.4461
Gastrointestinal	0.1015	0.1758	0.5777	1.7311
Brain	0.0296	0.1273	0.2322	4.3058
Hematopoietic	0.0535	0.0000	undef	0.0000
Skin	0.2166	0.0000	undef	0.0000
Hepatic	0.0809	0.1035	0.7813	1.2800
Heart	0.4133	0.2612	1.5825	0.6319
Testicles	0.0748	0.0468	1.5989	0.6254
Lung	0.1506	0.1227	1.2278	0.8145
Stomach-esophagus	0.2126	0.1073	1.9808	0.5048
Muscle-skeleton	0.0805	0.1680	0.4793	2.0863
Kidney	0.0543	0.0890	0.6100	1.6393
Pancreas	0.0562	0.1712	0.3281	3.0479
Penis	0.1497	0.2399	0.6240	1.6026
Prostate	0.0850	0.0362	2.3483	0.4258
Uterus-endometrium	0.0541	0.0000	undef	0.0000
Uterus-myometrium	0.0457	0.1019	0.4489	2.2276
Uterus-general	0.0560	0.0000	undef	0.0000
Breast hyperplasia	0.0991			
Prostate hyperplasia	0.0832			
Seminal vesicle	0.0801			
Sensory organs	0.1059			
White blood cells	0.0720			
Cervix	0.0639			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0835	Breast	0.0544
Gastrointestinal	0.0361	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0101
Hematopoietic	0.0433	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0466
Hepatic	0.0000	Gastrointestinal	0.0610
Heart-blood vessels	0.0961	Hematopoietic	0.0000
Lung	0.0867	Skin-muscle	0.0421
Suprarenal gland	0.0761	Testicles	0.0000
Kidney	0.0309	Lung	0.1474
Placenta	0.1151	Nerves	0.0110
Prostate	0.5984	Prostate	0.0205
Sensory organs	0.0251	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 123

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0017	0.0075	0.2264	4.4166
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0030	0.0021	1.4399	0.6945
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0010	0.0061	0.1693	5.9051
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0086	0.0060	1.4278	0.7004
Kidney	0.0027	0.0205	0.1322	7.5658
Pancreas	0.0066	0.0055	1.1966	0.8357
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0058	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0134
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0130
Lung	0.0254	Skin-muscle	0.0000
Suprarenal gland	0.0062	Testicles	0.0164
Kidney	0.0182	Lung	0.0030
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0125
		Uterus_n	

NORMAL
% freq

RATIOS
N/T T/N

FETUS
& freq.

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0030
Kidney t	0.0000
Ovary uterus	0.0000
Prostate_n	0.0121
Sensory Organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 259

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder			
Breast	0.0000	0.0000	undef undef
Large intestine	0.0117	0.0023	4.9785 0.2009
Small intestine	0.0070	0.0014	5.0097 0.1996
Ovary	0.0000	0.0057	0.0000 undef
Endocrine tissue	0.0082	0.0000	undef 0.0000
Brain	0.0000	0.0119	0.0000 undef
Skin	0.0032	0.0089	0.3621 2.7613
Hepatic	0.0006	0.0000	undef 0.0000
Heart	0.0037	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lung	0.0081	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0019	0.0000	undef 0.0000
Kidney	0.0145	0.0000	undef 0.0000
Pancreas	0.0000	0.0037	0.0000 undef
Prostate	0.0022	0.0000	undef 0.0000
T lymphoma	0.0017	0.0000	undef 0.0000
Uterus	0.0019	0.0000	undef 0.0000
White blood cells	0.0025	0.0075	0.3381 2.9576
Hematopoietic	0.0059	0.0138	0.4284 2.3344
Penis	0.0000	0.0000	undef undef
Seminal vesicle	0.0027		
Sensory organs	0.0080		
	0.0141		
	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0245
Fetal	0.0070
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0061
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 260

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0000	0.0000	undef undef
Breast	0.0000	0.0023	0.0000 undef
Large intestine	0.0062	0.0000	undef 0.0000
Small intestine	0.0019	0.0085	0.2243 4.4591
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0000	0.0525	0.0000 undef
Brain	0.0032	0.0071	0.4527 2.2091
Skin	0.0023	0.0020	1.1605 0.8617
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0063	0.0000 undef
Testicles	0.0051	0.0000	undef 0.0000
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0088	0.0037	2.3680 0.4223
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0017	0.0000	undef 0.0000
Pancreas	0.0022	0.0000	undef 0.0000
Prostate	0.0083	0.0000	undef 0.0000
T lymphoma	0.0028	0.0013	2.1706 0.4607
Uterus	0.0051	0.0224	0.2254 4.4364
White blood cells	0.0015	0.0000	undef 0.0000
Hematopoietic	0.0027	0.0304	0.0902 11.0896
Penis	0.0013		
Seminal vesicle	0.0000		
Sensory organs	0.0070		
	0.0000		

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0107
Adrenal gland	0.0036
Kidney	0.0000
Placenta	0.0062
Prostate	0.0000
Sensory organs	0.0000
	0.0251

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0098
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0060
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0113
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma				
Bladder				
Breast	0.0025	0.0000	undef	0.0000
Large intestine	0.0000	0.0000	undef	undef
Small intestine	0.0009	0.0014	0.6262	1.5969
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0027	0.0000	undef	0.0000
Brain	0.0000	0.0191	0.0000	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0006	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0055	0.0000	undef
T lymphoma	0.0019	0.0000	undef	0.0000
Uterus	0.0051	0.0000	undef	0.0000
White blood cells	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0034	0.0000	undef	0.0000
Penis	0.0013			
Seminal vesicle	0.0000			
Sensory organs	0.0070			
	0.0000			

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0188
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0023
Ovary uterus	0.0061
Prostate_n	0.0000
Sensory Organs	0.0000
White blood cells	

Seq.
NORMAL
% freq

TUMOR
& freq.

RATIOS
N/T T/N

B lymphoma
Bladder
Breast
Large intestine
Small intestine
Ovary
Endocrine tissue
Brain
Skin
Hepatic
Heart
Testicles
Lung
Stomach-esophagus
Muscle-skeleton
Kidney
Pancreas
Prostate
T lymphoma
Uterus
White blood cells
Hematopoietic
Penis
Seminal vesicle
Sensory organs

0.0150
0.0156
0.0158
0.0038
0.0110
0.0178
0.0064
0.0081
0.0110
0.0139
0.0193
0.0080
0.0175
0.0000
0.0017
0.0045
0.0132
0.0104
0.0101
0.0192
0.0055
0.0067
0.0080
0.0070
0.0118

0.0000
0.0023
0.0056
0.0028
0.0320
0.0334
0.0213
0.0060
0.0000
0.0190
0.0000
0.0118
0.0129
0.0064
0.0111
0.0096
0.0000
0.0091
0.0149
0.0230
0.0304

```
undef 0.0000
6.6380 0.1506
2.8179 0.3549
1.3456 0.7432
0.3435 2.9109
0.5333 1.8752
0.3018 3.3136
1.3539 0.7386
undef 0.0000
0.7324 1.3653
undef 0.0000
0.6786 1.4737
1.3531 0.7390
0.0000 undef
0.1546 6.4671
0.4642 2.1540
undef 0.0000
1.1370 0.8795
0.6762 1.4788
0.8353 1.1971
0.1803 5.5448
```

FETUS
& freq.

- Development
- Gastrointestinal
- Brain
- Hematopoietic
- Skin
- Hepatic
- Heart-blood vessels
- Lung
- Adrenal gland
- Kidney
- Placenta
- Prostate
- Sensory organs

0.0000
0.0056
0.0000
0.0275
0.0000
0.0000
0.0142
0.0000
0.0254
0.0124
0.0121
0.0000
0.0251

STANDARDIZED/SUBTRACTED LIBRARIES
0.0000 & frequency

Breast
Breast t
Large Intestine_t
Ovary n
Ovary_t
Endocrine tissue
Fetal
Gastrointestinal
Hematopoietic
Skin-muscle
Testicles n
Testicles_t
Lungs n
Lungs_t
Nerves
Kidney t
Ovary uterus
Prostate n
Sensory organs
White blood cells

0.0000
0.0000
0.0000
0.0000
0.0203
0.0000
0.0162
0.0122
0.0000
0.0454
0.0125
0.0000
0.0000
0.0000
0.0100
0.0000
0.0293
0.0000
0.0000
0.0000

Electronic Northern for Seq. ID: 263

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0125	0.0136	0.9198 1.0872
Breast	0.0039	0.0188	0.2075 4.8204
Large intestine	0.0114	0.0281	0.4070 2.4568
Small intestine	0.0211	0.0142	1.4801 0.6756
Ovary	0.0082	0.0000	undef 0.0000
Endocrine tissue	0.0089	0.0286	0.3111 3.2147
Brain	0.0161	0.0151	1.0599 0.9435
Skin	0.0211	0.0110	1.9234 0.5199
Hepatic	0.0110	0.0000	undef 0.0000
Heart	0.0046	0.0127	0.3662 2.7307
Testicles	0.0162	0.0000	undef 0.0000
Lung	0.0080	0.0178	0.4523 2.2108
Stomach-esophagus	0.0136	0.0111	1.2278 0.8145
Muscle-skeleton	0.0072	0.0128	0.5666 1.7648
Kidney	0.0158	0.0185	1.0206 0.9799
Pancreas	0.0157	0.0145	1.0831 0.9232
Prostate	0.0083	0.0221	0.3739 2.6743
T lymphoma	0.0123	0.0039	3.1352 0.3190
Uterus	0.0000	0.0149	0.0000 undef
White blood cells	0.0077	0.0230	0.3368 2.9694
Hematopoietic	0.0082	0.0000	undef 0.0000
Penis	0.0094		
Seminal vesicle	0.0107		
Sensory organs	0.0070		
	0.0235		

FETUS % freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0107
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0203
Endocrine tissue	0.0000
Fetal	0.0069
Gastrointestinal	0.0488
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0167
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0060
Kidney t	0.0000
Ovary uterus	0.0158
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

NORMAL	TUMOR	RATIOS	
% freq.	% freq.	N/T	T/N

	% freq.	% freq.	N/T I/N
B lymphoma			
Bladder	0.0150	0.0136	1.1037 0.9060
Breast	0.0273	0.0211	1.2907 0.7748
Large intestine	0.0229	0.0632	0.3618 2.7639
Small intestine	0.0268	0.0256	1.0466 0.9555
Ovary	0.0192	0.0000	undef 0.0000
Endocrine tissue	0.0089	0.0501	0.1778 5.6255
Brain	0.0193	0.0142	1.3580 0.7364
Skin	0.0041	0.0160	0.2539 3.9391
Hepatic	0.0073	0.0000	undef 0.0000
Heart	0.0465	0.0254	1.8311 0.5461
Testicles	0.0091	0.0412	0.2215 4.5144
Lung	0.0120	0.0000	undef 0.0000
Stomach-esophagus	0.0204	0.0185	1.1050 0.9049
Muscle-skeleton	0.0290	0.0384	0.7557 1.3233
Kidney	0.0069	0.0185	0.3711 2.6946
Pancreas	0.0537	0.0289	1.8570 0.5385
Prostate	0.0380	0.0110	3.4403 0.2907
T lymphoma	0.0330	0.0130	2.5323 0.3949
Uterus	0.0051	0.0075	0.6762 1.4788
White blood cells	0.0148	0.0138	1.0709 0.9338
Hematopoietic	0.0075	0.0000	undef 0.0000
Penis	0.0147		
Seminal vesicle	0.0054		
Sensory organs	0.0000		
	0.0235		

- Development
- Gastrointestinal
- Brain
- Hematopoietic
- Skin
- Hepatic
- Heart-blood vessels
- Lung
- Adrenal gland
- Kidney
- Placenta
- Prostate
- Sensory organs

Breast	0.0204
Breast t	0.0000
Large Intestine_t	0.0000
Ovary n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles n	0.0000
Testicles_t	0.0000
Lungs n	0.0000
Lungs_t	0.0040
Nerves	0.0000
Kidney t	0.0090
Ovary Uterus	0.0121
Prostate n	0.0000
Sensory Organs	0.0000
White blood cells	

NORMAL
% freq.

TUMOR
% freq.

RATIOS
N/T T/N

	0.0000	0.0272	0.0000 undef
B lymphoma	0.0117	0.0023	4.9785 0.2009
Bladder	0.0141	0.0155	0.9109 1.0979
Breast	0.0920	0.0968	0.9498 1.0528
Large intestine	0.0247	0.0000	undef 0.0000
Small intestine	0.0208	0.0882	0.2354 4.2478
Ovary	0.0016	0.0000	undef 0.0000
Endocrine tissue	0.0000	0.0010	0.0000 undef
Brain	0.0000	0.0000	undef undef
Skin	0.0000	0.0444	0.0000 undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0000	undef undef
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0165	0.0111	1.4909 0.6707
Muscle-skeleton	0.0362	0.0128	2.8338 0.3529
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0000	0.0166	0.0000 undef
T lymphoma	0.0207	0.0352	0.5895 1.6963
Uterus	0.0025	0.0000	undef 0.0000
White blood cells	0.0030	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0027		
Seminal vesicle	0.0000		
Sensory organs	0.0915		
	0.0118		

FETUS
& freq.

Development	0.0000
Gastrointestinal	0.0278
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0108
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES & frequency

Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0253
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0293
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0000
Ovary_uterus	0.0113
Prostate_n	0.0182
Sensory Organs	0.0000
White blood cells	0.0000

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma				
Bladder	0.0025	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Large intestine	0.0114	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0055	0.0000	undef	0.0000
Endocrine tissue	0.0059	0.0525	0.1131	8.8401
Brain	0.0161	0.0035	4.5268	0.2209
Skin	0.0017	0.0000	undef	0.0000
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0071	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0049	0.0037	1.3155	0.7601
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0470	0.0048	9.7491	0.1026
Prostate	0.0033	0.0000	undef	0.0000
T lymphoma	0.0019	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0044	0.0046	0.9638	1.0375
Hematopoietic	0.0007	0.0000	undef	0.0000
Penis	0.0000			
Seminal vesicle	0.0080			
Sensory organs	0.0000			

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0068
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0020
Nerves	0.0000
Kidney t	0.0023
Ovary uterus	0.0000
Prostate_n	0.0000
Sensory Organs	0.0000
White blood cells	

seq. 1
NORMAL
% freq.

TUMOR
% freq.

RATIOS
N/T T/N

	% freq.	% freq.	RATIO N/T T
B lymphoma			
Bladder			
Breast			
Large intestine	0.0050	0.0000	undef 0.0000
Small intestine	0.0000	0.0070	0.0000 undef
Ovary	0.0026	0.0014	1.8786 0.5323
Endocrine tissue	0.0000	0.0000	undef undef
Brain	0.0055	0.0000	undef 0.0000
Skin	0.0000	0.0119	0.0000 undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0029	0.0010	2.9013 0.3447
Testicles	0.0000	0.0394	0.0000 undef
Lung	0.0030	0.0000	undef undef
Stomach-esophagus	0.0040	0.0000	undef 0.0000
Muscle-skeleton	0.0049	0.0000	undef 0.0000
Kidney	0.0000	0.0000	undef 0.0000
Pancreas	0.0034	0.0000	undef undef
Prostate	0.0000	0.0000	undef 0.0000
T lymphoma	0.0000	0.0048	0.0000 undef
Uterus	0.0028	0.0000	undef undef
White blood cells	0.0000	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0007	0.0000	undef undef
Seminal vesicle	0.0000		undef 0.0000
Sensory organs	0.0054		
	0.0000		
	0.0000		

FETUS
& freq.

- Development
- Gastrointestinal
- Brain
- Hematopoietic
- Skin
- Hepatic
- Heart-blood vessels
- Lung
- Adrenal gland
- Kidney
- Placenta
- Prostate
- Sensory organs

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0010
Kidney_t	0.0000
Ovary_uterus	0.0023
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma				
Bladder	0.0025	0.0000	undef	0.0000
Breast	0.0117	0.0094	1.2446	0.8035
Large intestine	0.0088	0.0253	0.3479	2.8744
Small intestine	0.0192	0.0028	6.7278	0.1486
Ovary	0.0192	0.0213	0.9018	1.1089
Endocrine tissue	0.0030	0.0143	0.2074	4.8219
Brain	0.0193	0.0035	5.4321	0.1841
Skin	0.0081	0.0249	0.3249	3.0774
Hepatic	0.0184	0.0000	undef	0.0000
Heart	0.0093	0.0063	1.4649	0.6826
Testicles	0.0112	0.0000	undef	0.0000
Lung	0.0040	0.0118	0.3393	2.9475
Stomach-esophagus	0.0126	0.0037	3.4204	0.2924
Muscle-skeleton	0.0072	0.0000	undef	0.0000
Kidney	0.0120	0.0037	3.2472	0.3080
Pancreas	0.0157	0.0048	3.2497	0.3077
Prostate	0.0050	0.0110	0.4487	2.2285
T lymphoma	0.0104	0.0052	1.9897	0.5026
Uterus	0.0051	0.0000	undef	0.0000
White blood cells	0.0163	0.0092	1.7670	0.5659
Hematopoietic	0.0110	0.0000	undef	0.0000
Penis	0.0027			
Seminal vesicle	0.0054			
Sensory organs	0.0000			
	0.0000			

Development	0.0139
Gastrointestinal	0.0056
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0122
Hematopoietic	0.0257
Skin-muscle	0.0032
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0010
Nerves	0.0000
Kidney_t	0.0023
Ovary Uterus	0.0243
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder			
Breast	0.0025	0.0000	undef 0.0000
Large intestine	0.0156	0.0047	3.3190 0.3013
Small intestine	0.0079	0.0014	5.6359 0.1774
Ovary	0.0096	0.0057	1.6820 0.5945
Endocrine tissue	0.0000	0.0000	undef undef
Brain	0.0030	0.0191	0.1555 6.4291
Skin	0.0064	0.0018	3.6214 0.2761
Hepatic	0.0058	0.0060	0.9671 1.0340
Heart	0.0037	0.0000	undef 0.0000
Testicles	0.0000	0.0127	0.0000 undef
Lung	0.0091	0.0000	undef 0.0000
Stomach-esophagus	0.0080	0.0000	undef 0.0000
Muscle-skeleton	0.0068	0.0037	1.8417 0.5430
Kidney	0.0000	0.0064	0.0000 undef
Pancreas	0.0034	0.0111	0.3093 3.2335
Prostate	0.0045	0.0000	undef 0.0000
T lymphoma	0.0083	0.0110	0.7479 1.3371
Uterus	0.0057	0.0117	0.4823 2.0732
White blood cells	0.0025	0.0000	undef 0.0000
Hematopoietic	0.0044	0.0092	0.4819 2.0750
Penis	0.0034	0.0000	undef 0.0000
Seminal vesicle	0.0027		
Sensory organs	0.0188		
	0.0141		
	0.0118		

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0000
Hematopoietic	0.0032
Skin-muscle	0.0000
Testicles n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0020
Nerves	0.0000
Kidney t	0.0068
Ovary uterus	0.0000
Prostate n	0.0077
Sensory Organs	0.0000
White blood cells	

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder			
Breast	0.0075	0.0000	undef 0.0000
Large intestine	0.0156	0.0047	3.3190 0.3013
Small intestine	0.0167	0.0197	0.8499 1.1767
Ovary	0.0307	0.0199	1.5378 0.6503
Endocrine tissue	0.0082	0.0213	0.3865 2.5875
Brain	0.0059	0.0334	0.1778 5.6255
Skin	0.0321	0.0248	1.2934 0.7732
Hepatic	0.0365	0.0170	2.1504 0.4650
Heart	0.0257	0.0000	undef 0.0000
Testicles	0.0000	0.0127	0.0000 undef
Lung	0.0426	0.0000	undef 0.0000
Stomach-esophagus	0.0161	0.0118	1.3571 0.7369
Muscle-skeleton	0.0272	0.0222	1.2278 0.8144
Kidney	0.0072	0.0000	undef 0.0000
Pancreas	0.0137	0.0074	1.8555 0.5389
Prostate	0.0246	0.0145	1.7022 0.5875
T lymphoma	0.0050	0.0000	undef 0.0000
Uterus	0.0179	0.0065	2.7494 0.3637
White blood cells	0.0177	0.0672	0.2630 3.8026
Hematopoietic	0.0118	0.0046	2.5703 0.3891
Penis	0.0219	0.0000	undef 0.0000
Seminal vesicle	0.0147		
Sensory organs	0.0188		
	0.0281		
	0.0000		

Development	0.0000
Gastrointestinal	0.0167
Brain	0.0188
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0356
Lung	0.0108
Adrenal gland	0.0254
Kidney	0.0124
Placenta	0.0182
Prostate	0.0249
Sensory organs	0.0000

Breast	0.0068
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0110
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0227
Testicles_n	0.0125
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0281
Kidney_t	0.0000
Ovary_uterus	0.0068
Prostate_n	0.0061
Prostate_t	0.0232
Sensory organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 271

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0125	0.0407	0.3066 3.2617
Breast	0.0117	0.0164	0.7112 1.4061
Large intestine	0.0123	0.0098	1.2524 0.7985
Small intestine	0.0057	0.0057	1.0092 0.9909
Ovary	0.0165	0.0000	undef 0.0000
Endocrine tissue	0.0030	0.0143	0.2074 4.8219
Brain	0.0096	0.0195	0.4938 2.0250
Skin	0.0122	0.0070	1.7408 0.5745
Hepatic	0.0110	0.0000	undef 0.0000
Heart	0.0093	0.0000	undef 0.0000
Testicles	0.0071	0.0137	0.5169 1.9347
Lung	0.0201	0.0059	3.3928 0.2947
Stomach-esophagus	0.0117	0.0148	0.7893 1.2669
Muscle-skeleton	0.0072	0.0320	0.2267 4.4110
Kidney	0.0086	0.0000	undef 0.0000
Pancreas	0.0045	0.0096	0.4642 2.1540
Prostate	0.0017	0.0055	0.2992 3.3427
T lymphoma	0.0066	0.0117	0.5627 1.7770
Uterus	0.0126	0.0149	0.8453 1.1830
White blood cells	0.0059	0.0322	0.1836 5.4469
Hematopoietic	0.0062	0.0304	0.2029 4.9287
Penis	0.0107		
Seminal vesicle	0.0000		
Sensory organs	0.0141		
	0.0235		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0250
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0220
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0421
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0211
Nerves	0.0000
Kidney t	0.0248
Ovary uterus	0.0000
Prostate_n	0.0232
Sensory organs	0.0000
White blood cells	

NORMAL
& freq.

RATIOS
N/T T/N

FETUS
& freq.

STANDARDIZED/SUBTRACTED LIBRARIES & frequency

Breast	0.0136
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0052
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0195
Lungs_n	0.0000
Lungs_t	0.0121
Nerves	0.0000
Kidney t	0.0000
Ovary Uterus	0.0061
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 273

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0025	0.0000	undef 0.0000
Breast	0.0078	0.0188	0.4149 2.4104
Large intestine	0.0079	0.0112	0.7045 1.4195
Small intestine	0.0019	0.0057	0.3364 2.9727
Ovary	0.0055	0.0000	undef 0.0000
Endocrine tissue	0.0030	0.0215	0.1383 7.2328
Brain	0.0080	0.0053	1.5089 0.6627
Skin	0.0041	0.0070	0.5803 1.7234
Hepatic	0.0147	0.0000	undef 0.0000
Heart	0.0046	0.0000	undef 0.0000
Testicles	0.0203	0.0000	undef 0.0000
Lung	0.0000	0.0355	0.0000 undef
Stomach-esophagus	0.0039	0.0111	0.3508 2.8506
Muscle-skeleton	0.0145	0.0128	1.1335 0.8822
Kidney	0.0120	0.0074	1.6236 0.6159
Pancreas	0.0000	0.0048	0.0000 undef
Prostate	0.0000	0.0276	0.0000 undef
T lymphoma	0.0085	0.0065	1.3023 0.7679
Uterus	0.0303	0.0149	2.0287 0.4929
White blood cells	0.0133	0.0092	1.4458 0.6917
Hematopoietic	0.0205	0.0000	undef 0.0000
Penis	0.0027		
Seminal vesicle	0.0054		
Sensory organs	0.0000		
	0.0118		

FETUS % freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0063
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0213
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0068
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0152
Fetal	0.0245
Gastrointestinal	0.0023
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0060
Kidney_t	0.0000
Ovary Uterus	0.0090
Prostate_n	0.0000
Sensory Organs	0.0000
White blood cells	0.0000

2.2. Fisher Test

In order to decide whether a partial sequence *S* of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to *S*. If the null hypothesis can be rejected with high enough certainty, the gene belonging to *S* is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

Example 3

Automatic lengthening of the partial sequence

Automatic lengthening of partial sequence *S* is completed in three steps:

1. Determination of all sequences homologous to *S* from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence *C* from the assembled sequences.

The consensus sequence *C* will generally be longer than initial sequence *S*. Its electronic Northern Blot will

accordingly deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences C_i (i : iteration index) obtained in each case until the alternative hypothesis is rejected (if H_0 Exit; truncation criterion I) or until automatic lengthening is no longer possible (while $C_i > C_{i-1}$; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from ovarian tumor tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORFs) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

Mapping of nucleic acid sequences on the human genome

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server (http://www.stanford.edu/RH/rhserver_form2.html). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the gap between genome mapping and genome sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence mapping by electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,

the results were evaluated with the above-mentioned software and the software of the Whitehead Institute
(<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

Example 5

Obtaining genomic DNA sequences (BAC clones)

The genomic BAC clones that contain the corresponding cDNAs (<http://www.tree.caltech.edu/>; Shizuya, H.; B. Birren, U-J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, M. Simon (1992) Proc. Natl. Acad. Sci., USA 89: 8794-8797) were isolated with the procedure of "down-to-the-well." In this procedure, a library consisting of BAC clones (the library covers roughly 3x the human genome) is moved into a certain raster, so that the DNA of these clones with a specific PCR can be studied. In doing so, "pooling" of the DNA of different BAC clones takes place. Combinatorial analysis makes it possible to determine the clones that contain the desired DNA. By fixing the clones, the address of the clones in the library can be determined. This address together with the name of the library which is being used unequivocally fixes the clones and thus the DNA sequence of these clones.

The following examples explain the successful isolation of the genomic BAC clones without limiting them thereto.

The libraries used were CITB B and CITB C:

Seq. ID No.

Identified BACs

4	195/N/3	206/P/3	384/I/3	323/G/9	
5	222/B/10	404/E/10	526/F/20	565/P/11	279/F/14
9	501/L/21				
11	490/P/4	321/I/23	410/F/5	443/N/20	
19	311/A/19	505/F/17	216/D/8	219/C/22	
29	382/N/10	539/L/7			
31	530/D/11				
35	503/N/10				
37	547/D/16	215/P/16	439/K/6		
39	216/L/9	512/F/5	203/J/15		
45	205/K/7	250/H/22	283/C/17	528/B/20	402/L/11
80	371/A/20	470/L/3	495/L/3		
92	254/M/9	376/O/12	421/L/18	429/J/19	
112	243/O/14	520/K/15	565/J/17	565/J/24	

TABLE I

Col. 1 - Seq. ID No.
Col. 2 - Expression
Col. 3 - Function
Col. 4 - Modules
Col. 5 - Cytogenetic localization
Col. 6 - Nearest marker

TABLE I

Seq. ID No.	Expression	Function
1	Overexpressed in ovarian tumor tissue	Unknown
2	Overexpressed in ovarian tumor tissue	Unknown
3	Overexpressed in ovarian tumor tissue	Unknown
4	Overexpressed in ovarian tumor tissue	P52r1PK
5	Overexpressed in ovarian tumor tissue	Unknown
6	Overexpressed in ovarian tumor tissue	Unknown
7	Overexpressed in ovarian tumor tissue	Unknown
8	Overexpressed in ovarian tumor tissue	Unknown
9	Overexpressed in ovarian tumor tissue	Unknown
10	Overexpressed in ovarian tumor tissue	Unknown
12	Overexpressed in ovarian tumor tissue	Unknown
13	Overexpressed in ovarian tumor tissue	Unknown
15	Overexpressed in ovarian tumor tissue	Unknown
16	Overexpressed in ovarian tumor tissue	Unknown
18	Overexpressed in ovarian tumor tissue	Unknown
19	Overexpressed in ovarian tumor tissue	Unknown

TABELLE I

Seq ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
1	in Ovariumorgewebe überexprimiert	unbekannt		1p31.1-p34.1	SHGC-2542,2540,2456; D1S448-D1S500;; WI-6555; D1S198-D1S462
2	in Ovariumorgewebe überexprimiert	unbekannt		2p22.3-p23.3	SGC32173; D2S174-D2S390;; TIGR-A006H24;D2S392-D2S390
3	in Ovariumorgewebe überexprimiert	unbekannt		4p15.1	WI-15951 (D4S1043-SHGC-16179)
4	in Ovariumorgewebe überexprimiert	P52RIPK		11q13.5 - q14.1	SHGC-31396 (SHGC-32287, D11S4681)
5	in Ovariumorgewebe überexprimiert	unbekannt		1q22	SHGC-31641
6	in Ovariumorgewebe überexprimiert	unbekannt		13q33.1 - q34	AFM310yd5
7	in Ovariumorgewebe überexprimiert	unbekannt		8q11.23-q12.1	SHGC-32002; D8S1828-D8S507
8	in Ovariumorgewebe überexprimiert	unbekannt		4q24	SHGC-36699
9	in Ovariumorgewebe überexprimiert	unbekannt	PRO_RICH	2q35	SHGH-32531 (D2S1297, SHGC-35278)
10	in Ovariumorgewebe überexprimiert	unbekannt	PHD		
12	in Ovariumorgewebe überexprimiert	unbekannt		5q23.3-q31.1	AFM200ya9=D5S414
13	in Ovariumorgewebe überexprimiert	unbekannt		3p23	WI-6841;D3S1599-D3S1583
15	in Ovariumorgewebe überexprimiert	unbekannt		6q22.1-q24.3	SHGC-33316; D6S453-D6S311
16	in Ovariumorgewebe überexprimiert	unbekannt	NLS_BP	10p15.3	CDa1lh03; D10S533-D10S594;; SHGC-11812; D10S558-D10S591
18	in Ovariumorgewebe überexprimiert	unbekannt	Ribosomal_L24e	15q21.3-q22.1	Cda17g12; D15S209-D15S198
19	in Ovariumorgewebe überexprimiert	unbekannt		11q14.3	SHGC-36010 (D11S1979, D11S1887)

Seq. ID No.	Expression	Function
20	Overexpressed in ovarian tumor tissue	Unknown
21	Overexpressed in ovarian tumor tissue	Unknown
22	Overexpressed in ovarian tumor tissue	Unknown
23	Overexpressed in ovarian tumor tissue	Unknown
24	Overexpressed in ovarian tumor tissue	Unknown
25	Overexpressed in ovarian tumor tissue	Branchio-oto-renal syndrome candidate gene
26	Overexpressed in ovarian tumor tissue	Unknown
27	Overexpressed in ovarian tumor tissue	Unknown
28	Overexpressed in ovarian tumor tissue	Unknown
29	Overexpressed in ovarian tumor tissue	Unknown
30	Overexpressed in ovarian tumor tissue	Unknown
31	Overexpressed in ovarian tumor tissue	Unknown
32	Overexpressed in ovarian tumor tissue	Partially homologous to R. norvegicus calpain
33	Overexpressed in ovarian tumor tissue	Partially homologous to human mRNA for fungal sterol-C5-desaturase homolog
34	Overexpressed in ovarian tumor tissue	Partially homologous to human GPx-3 mRNA for plasma glutathione peroxidase
35	Overexpressed in ovarian tumor tissue	Partially homologous to homo sapiens CHD2 mRNA

Seq ID No.	Expression	Funktion	Module	Cylogenetische Lokalisation	nearest marker
20	in Ovariumorgewebe überexprimiert	unbekannt		3q22.2-3q22.3	SHGC-34629 (SHGC-30855, SGC32794)
21	in Ovariumorgewebe überexprimiert	unbekannt		3q26.33-q29	AFM308y1 (D3S2363, D3S3669)
22	in Ovariumorgewebe überexprimiert	unbekannt		7q11.23	SHGC-37054
23	in Ovariumorgewebe überexprimiert	unbekannt			
24	in Ovariumorgewebe überexprimiert	unbekannt		4q28.1-q31.1	WI-30941;SGC30941; D4S1580-D4S427
25	in Ovariumorgewebe überexprimiert	Branchio-oto-renal syndrome candidate gene		7q32.3-q33	AFMc024we9
26	in Ovariumorgewebe überexprimiert	unbekannt	NLS_BP	17q23.3	SHGC-64257
27	in Ovariumorgewebe überexprimiert	unbekannt		17p12-p13.2	SHGC-31370 (SHGC-35547-SHGC-35513)
28	in Ovariumorgewebe überexprimiert	unbekannt		10q22.3	Cda0wf11, TIGR-A001X23;D10S607-D10S201
29	in Ovariumorgewebe überexprimiert	unbekannt		11q13.2-q13.5	WI-14303; D11S4136-D11S1314;; TIGR-A005U01; D11S913-D11S1314/RH;SHGC-14407
30	in Ovariumorgewebe überexprimiert	unbekannt		7p21.3	SHGC-14339
31	in Ovariumorgewebe überexprimiert	unbekannt		12p12.3	AFMb320va9
32	in Ovariumorgewebe überexprimiert	Partielles Homolog zu R. norvegicus calpain		1q41	SHGC-3992 (D1S2550-D1S2568)
33	in Ovariumorgewebe überexprimiert	Partiell Homolog zu Human mRNA for fungal sterol-C5-desaturase homolog	Thymosin	11q23.3	WI-19895; D11S924-D11S925
34	in Ovariumorgewebe überexprimiert	Partiell homolog zu Human GPx-3 mRNA for plasma glutathione peroxidase	GSHPx	5q33.1	SHGC-10972
35	in Ovariumorgewebe überexprimiert	Partiell Homolog zu Homo sapiens CHD2 mRNA		19q13.13 - q13.2	AFMb018wh1

Seq. ID No.	Expression	Function
36	Overexpressed in ovarian tumor tissue	Human homolog to M. musculus formin binding protein 21
38	Overexpressed in ovarian tumor tissue	Human homolog to Tribolium castaneum zinc finger protein
39	Overexpressed in ovarian tumor tissue	Human homolog to S. cerevisiae chromosome II sequence for ORF YBR1725
40	Overexpressed in ovarian tumor tissue	Human homolog to Rattus norvegicus rsly 1p
41	Overexpressed in ovarian tumor tissue	Human homolog to PEC-60=gastrointestinal peptide, swine
42	Overexpressed in ovarian tumor tissue	Human homolog to Mus musculus mCAF1 protein
43	Overexpressed in ovarian tumor tissue	Human homolog to Mouse mitochondrial genome; unidentified reading frame
44	Overexpressed in ovarian tumor tissue	Human homolog to Mouse kidney androgen-regulated protein (KAP)
45	Overexpressed in ovarian tumor tissue	Human homolog to M. musculus Tera
46	Overexpressed in ovarian tumor tissue	Human homolog to Caenorhabditis elegans cosmid T27F7
47	Overexpressed in ovarian tumor tissue	Human homolog to Caenorhabditis elegans cosmid T27F7
48	Overexpressed in ovarian tumor tissue	Human homolog to Caenorhabditis elegans cosmid K11H12
49	Overexpressed in ovarian tumor tissue	Human homolog to Caenorhabditis elegans cosmid C43E11

Seq ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
36	in Ovariumorgewebe überexprimiert	Humanes Homolog zu M. musculus formin binding protein 21	WW_rsp5_WWP		
38	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Tribolium castaneum zinc finger protein		2p13.1- p16.1;RH: 2p13.1-p13.3	slSG31094; D2S292-D2S145
39	in Ovariumorgewebe überexprimiert	Humanes Homolog zu S. cerevisiae chromosome II sequence for ORF YBR1725		19q12	AFM205y110 (D19S1080, D19S590)
40	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Rattus norvegicus rsly1p	Sec1	17	
41	in Ovariumorgewebe überexprimiert	Humanes Homolog zu PEC-60=gastrointestinal peptide, swine	kazal		
42	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Mus musculus mCAF1 protein		8p22-p23.3	BDA16f11; D8S549-D8S1733 bzw. S280
43	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Mouse mitochondrial genome; Unidentified reading frame	oxidored_q1_N		
44	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Mouse kidney androgen-regulated protein (KAP)		1p36.31-p36.13	SHGC-11461 (D1S2565, SGC32561)
45	in Ovariumorgewebe überexprimiert	Humanes Homolog zu M. musculus Tera		12p11.21- p11.23	SHGC-1349 (D1S1621/D1S1805)
46	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid T27F7		19q13.33-qter	SHGC-30173; D19S418-qTEL
47	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid T27F7	PRO_RICH	2p11.1-p11.2	D2S388-D2S2181
48	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid K11H12	UPF0005	10q23.1	SHGC-167+SHGC-11466; D10S551-D10S532
49	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid C43E11	PRO_RICH	Xq22.3-Xq25	slSG2963; DXS1059-DXS1047

Seq. ID No.	Expression	Function
50	Overexpressed in ovarian tumor tissue	Human homolog to <i>Caenorhabditis elegans</i> cosmid C40H1
51	Overexpressed in ovarian tumor tissue	Human homolog to <i>C. elegans</i> cosmid K02D10
52	Overexpressed in ovarian tumor tissue	Human homolog to bovine inorganic pyrophosphatase
53	Overexpressed in ovarian tumor tissue	Human homolog to <i>B. laurus</i> mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex
54	Overexpressed in ovarian tumor tissue	Human homolog to <i>Aplysia californica</i> vesicle-associated membrane protein/synaptobrevin binding protein or others
55	Overexpressed in ovarian tumor tissue	Human homolog to <i>Aplysia californica</i> vesicle-associated membrane protein/synaptobrevin binding protein
56	Overexpressed in ovarian tumor tissue	Human homolog of <i>R. norvegicus</i> intestinal epithelium proliferating cell-associated mRNA sequence
57	Overexpressed in ovarian tumor tissue	Homologous to Bruton's tyrosine kinase
58	Overexpressed in ovarian tumor tissue	dbpB-like protein
59	Overexpressed in ovarian tumor tissue	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein
63	Overexpressed in ovarian tumor tissue	Protease, serine, 2 (trypsin 2)
65	Overexpressed in ovarian tumor tissue	Human annexin IV
67	Overexpressed in ovarian tumor tissue	Human X2 box repressor

Seq ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
50	in Ovariumgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid C40H1		1q22	WI-7155
51	in Ovariumgewebe überexprimiert	Humanes Homolog zu C. elegans cosmid K02D10		7p11.2-p12.3	Cda1bc08;D7S506-D7S499.; SHGC-17265+11581;D7S499-D7S2429
52	in Ovariumgewebe überexprimiert	Humanes Homolog zu Bovine inorganic pyrophosphatase	Pyrophosphatase	3q26.1	SHGC-9372
53	in Ovariumgewebe überexprimiert	Humanes Homolog zu B.taurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex		3q13.12-q13.2	D3S1310-D3S1575
54	in Ovariumgewebe überexprimiert	Humanes Homolog zu Aplysia californica vesicle-associated membrane protein/synaptobrevin binding protein aber anders		20q13.33	SHGC-11512
55	in Ovariumgewebe überexprimiert	Humanes Homolog zu Aplysia californica vesicle-associated membrane protein/synaptobrevin binding protein	PRO_RICH; MSP_DOMAIN	15q25.3-15q26.1	SHGC-69080 (D15S202/D15S1046, D15S1178)
56	in Ovariumgewebe überexprimiert	Humanes Homolog des R. norvegicus intestinal epithelium proliferating cell-associated mRNA sequence	PRO_RICH	1p32.2-p31.2	SGC34409
57	in Ovariumgewebe überexprimiert	Homolog zu Bruton's tyrosine kinase	rrm; PRO_RICH	10q21.1-q22.1	WI-11265; D10S581-D10S210
58	in Ovariumgewebe überexprimiert	dbpB-like protein	CSD; PRO_RICH	15q25.3-15q26.1	AFM282wg5=D15S202 (D15S1046;D15S1187)
59	in Ovariumgewebe überexprimiert	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	PRO_RICH	2p25.2-p25.1	
63	in Ovariumgewebe überexprimiert	Protease, serine, 2 (trypsin 2)	trypsin	7q35	SHGC-16894
65	in Ovariumgewebe überexprimiert	Humanes Annexin IV	annexin	2p13.1-p16.1	SHGC-9858
67	in Ovariumgewebe überexprimiert	Human X2 box repressor		16q12.1-q22.1	WI-6174; D16S408-D16S3089.;Cda01g10; D16S419-D16S415

Seq. ID No.	Expression	Function
68	Overexpressed in ovarian tumor tissue	Human transcriptional coactivator PC4
69	Overexpressed in ovarian tumor tissue	Human tetratricopeptide repeat protein
70	Overexpressed in ovarian tumor tissue	Human tax1-binding protein TXBP151
72	Overexpressed in ovarian tumor tissue	Human prothymosin alpha
73	Overexpressed in ovarian tumor tissue	Human profilin
74	Overexpressed in ovarian tumor tissue	Human pepsinogen C
76	Overexpressed in ovarian tumor tissue	Human osteopontin
78	Overexpressed in ovarian tumor tissue	Human non-histone chromosomal protein
79	Overexpressed in ovarian tumor tissue	Human mRNA for protein disulfide isomerase-related protein P5
80	Overexpressed in ovarian tumor tissue	Human mRNA for KIAA0332
81	Overexpressed in ovarian tumor tissue	Human mRNA for KIAA0078
82	Overexpressed in ovarian tumor tissue	Human mRNA for 90-kDa heat-shock protein
83	Overexpressed in ovarian tumor tissue	Human major nuclear matrix protein
84	Overexpressed in ovarian tumor tissue	Human Ku (p70/p80) subunit
85	Overexpressed in ovarian tumor tissue	Human interferon-induced 17-kDa/15-kDa protein
86	Overexpressed in ovarian tumor tissue	Human hsc70 gene for 71 kd heat shock cognate protein
88	Overexpressed in ovarian tumor tissue	Human gamma-interferon-inducible protein (IP-30)

Seq ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
68	in Ovariumorgewebe überexprimiert	Human transcriptional coactivator PC4		5p15.1	SGC32812; D5S477-D5S651
69	in Ovariumorgewebe überexprimiert	Human tetralricopeptide repeat protein		5q33.2-q33.3	TIGR-A002Q13; D5S412-D5S422
70	in Ovariumorgewebe überexprimiert	Human tax1-binding protein TXBP151		7p14.1-p21.3	SGC31789; D7S516-D7S632
72	in Ovariumorgewebe überexprimiert	Human prolthymosin alpha			
73	in Ovariumorgewebe überexprimiert	Human profilin	profilin	17p13.3	
74	in Ovariumorgewebe überexprimiert	Human pepsinogen C	asp	6p21.1	SGC35331; D6S426-D6S271
76	in Ovariumorgewebe überexprimiert	Human osteopontin	Osteopontin	4q13.3-q22.1	SHGC-9669; D4S1542-D4S1544
78	in Ovariumorgewebe überexprimiert	Human non-histone chromosomal protein	HMG14_17	21q22.3	
79	in Ovariumorgewebe überexprimiert	Human mRNA for protein disulfide isomerase-related protein P5	thioredo	2p23.3-p24.1	SGC31703; D2S287-D2S131; sISG1958; D2S162-D2S287
80	in Ovariumorgewebe überexprimiert	Human mRNA for KIAA0332		3p21.1	SHGC-14798 (D3S4210, SHGC-11985)
81	in Ovariumorgewebe überexprimiert	Human mRNA for KIAA0078	PRO_RICH		SHGC-9647; D7S651-D7S477; WI-14191; D8S269-D8S1799 +2 weitere auf Chr.8
82	in Ovariumorgewebe überexprimiert	Human mRNA for 90-kDa heat-shock protein	HSP90	4, 11, 1, 6	SHGC-11305
83	in Ovariumorgewebe überexprimiert	Human major nuclear matrix protein	RBD; ZF_MATRIN	5q31.1	SHGC-3183
84	in Ovariumorgewebe überexprimiert	Human Ku (p70/p80) subunit		2q34-q35	SHGC-11966; D2S2382-D2S164; WI-8140; D2S143-D2S164
85	in Ovariumorgewebe überexprimiert	Human interferon-induced 17-kDa/15-kDa protein	ubiquitin	1p36.31-p36.32	
86	in Ovariumorgewebe überexprimiert	Human hsc70 gene for 71 kd heat shock cognate protein	HSP70	11q23.3-q25	D20S113-D20S97
88	in Ovariumorgewebe überexprimiert	Human gamma-interferon-inducible protein (IP-30)		19p13.13	SHGC-32638; D19S899-D19S407

Seq. ID No.	Expression	Function
89	Overexpressed in ovarian tumor tissue	Human fatty acid binding protein homolog (PA-FABP)
90	Overexpressed in ovarian tumor tissue	Human enhancer of rudimentary homolog
91	Overexpressed in ovarian tumor tissue	Human deleted in split hand/split foot 1 (DSS1)
92	Overexpressed in ovarian tumor tissue	Human decay-accelerating factor mRNA
93	Overexpressed in ovarian tumor tissue	Human chromosome segregation gene homolog CAS
94	Overexpressed in ovarian tumor tissue	Human carcinoma-associated antigen GA733-2, human epithelial glycoprotein (EGP)
95	Overexpressed in ovarian tumor tissue	Human calmodulin
96	Overexpressed in ovarian tumor tissue	Human Bax alpha
97	Overexpressed in ovarian tumor tissue	HUMAN antileukoprotease (ALP)
98	Overexpressed in ovarian tumor tissue	Homo sapiens UDP-galactose-4-epimerase
99	Overexpressed in ovarian tumor tissue	Homo sapiens mRNA for putative progesterone binding protein
100	Overexpressed in ovarian tumor tissue	Homo sapiens mRNA for galectin-3
101	Overexpressed in ovarian tumor tissue	Homo sapiens monocyte/macrophage 1g-related receptor MIR-7 (MIR cl-7)
102	Overexpressed in ovarian tumor tissue	Homo sapiens Kunitz-type protease inhibitor
103	Overexpressed in ovarian tumor tissue	Homo sapiens hCPE-R mRNA for CPE-receptor
105	Overexpressed in ovarian tumor tissue	Homo sapiens DNA for amyloid precursor protein
106	Overexpressed in ovarian tumor tissue	Homo sapiens CD24 signal transducer

Seq ID No.	Expression	Funktion	Module	Cylogenetische Lokalisation	nearest marker
89	in Ovariumorgewebe überexprimiert	Human fatty acid binding protein homologue (PA-FABP)		17p11.2	SHGC-9883
90	in Ovariumorgewebe überexprimiert	Human enhancer of rudimentary homolog	ER	14q22.3-q24.2	WI-8921; D14S63-D14S251
91	in Ovariumorgewebe überexprimiert	Human deleted in split hand/split foot 1 (DSS1)		7q21.3-q22.1	D5S1977-D5S428 (Hs.85215)
92	in Ovariumorgewebe überexprimiert	Human decay-accelerating factor mRNA		1q32.2	SHGC-11228
93	in Ovariumorgewebe überexprimiert	Human chromosome segregation gene homolog CAS	IBN_NT	20q13	
94	in Ovariumorgewebe überexprimiert	Human carcinoma-associated antigen GA733-2, Human epithelial glycoprotein (EGP)	thyroglobulin_1	2p15-p21	AA113218; D2S119-D2S337
95	in Ovariumorgewebe überexprimiert	Human calmodulin	EF_HAND_2	2p16.3-p21	WI-9106; D2S391-D2S123
96	in Ovariumorgewebe überexprimiert	Human Bax alpha	Bcl-2	19q13.3-q13.4	
97	in Ovariumorgewebe überexprimiert	Human antileukoprotease (ALP)	wap	20q13.13-q13.2	WI-6969 (D20S880, SGC34003)
98	in Ovariumorgewebe überexprimiert	Homo sapiens UDP-galactose-4-epimerase	3Beta_HSD	1p36.11	SHGC-11459 (RH420-D1S3295)
99	in Ovariumorgewebe überexprimiert	Homo sapiens mRNA for putative progesterone binding protein		4q31.1	SHGC4-275
100	in Ovariumorgewebe überexprimiert	Homo sapiens mRNA for galeclin-3	Gal-bind_lectin	14q12-q22.3	D14S276-D14S66
101	in Ovariumorgewebe überexprimiert	Homo sapiens monocyte/macrophage Ig-related receptor MIR-7 (MIR cl-7)	7Im_1; G_PROTEIN_RECEPT OR_2; PRO_RICH	12q14.2-q14.3	SHGC-33073
102	in Ovariumorgewebe überexprimiert	Homo sapiens Kunitz-type protease inhibitor	Kunitz_BPTi;	19q13.2	TIGR-A007F08; D19S421-D19S408
103	in Ovariumorgewebe überexprimiert	Homo sapiens hCPE-R mRNA for CPE-receptor	PRO_RICH	7q11.23	
105	in Ovariumorgewebe überexprimiert	Homo sapiens DNA for amyloid precursor protein	Kunitz_BPT	21q21.2-q22.11	WI-8962; D21S265-D21S260
106	in Ovariumorgewebe überexprimiert	Homo sapiens CD24 signal transducer		6p21	AFM115xh2; SHGC-13799 - SHGC-32498

Seq. ID No.	Expression	Function
107	Overexpressed in ovarian tumor tissue	Homo sapiens Arp2/3 protein complex subunit p16-Arc (ARC16)
108	Overexpressed in ovarian tumor tissue	Histone H2B
110	Overexpressed in ovarian tumor tissue	H. sapiens, gene for membrane cofactor protein
111	Overexpressed in ovarian tumor tissue	H. sapiens TROP-2 gene
112	Overexpressed in ovarian tumor tissue	H. sapiens mRNA for Icin protein
113	Overexpressed in ovarian tumor tissue	H. sapiens mRNA for BiP protein
114	Overexpressed in ovarian tumor tissue	H. sapiens HE4 mRNA for extracellular proteinase inhibitor homolog
115	Overexpressed in ovarian tumor tissue	H. sapiens for neutrophil gelatinase associated lipocalin
116	Overexpressed in ovarian tumor tissue	H. sapiens mRNA for Sm protein G
117	Overexpressed in ovarian tumor tissue	H. sapiens for glutathione peroxidase-GI
120	Overexpressed in ovarian tumor tissue	CDC28 protein kinase 2
121	Overexpressed in ovarian tumor tissue	B-factor, properdin
122	Overexpressed in ovarian tumor tissue	Annexin II
123	Overexpressed in ovarian tumor tissue	ADP-ribosylation factor like 1
258	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 2
259	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 3

Seq ID No.	Expression	Funktion	Module	Cylogenetische Lokalisation	nearest marker
107	in Ovariumorgewebe überexprimiert	Homo sapiens Arp2/3 protein complex subunit p16-Arc (ARC16)		1q31.1	SHGC-58249(D1S2602/WI-2775,WI-7265)
108	in Ovariumorgewebe überexprimiert	Histone H2B	histone; Archaeal_histone	6p21.2-p21.31	WI-11733; D6S276-D6S439
110	in Ovariumorgewebe überexprimiert	H.sapiens, gene for Membrane cofactor protein	sushi	1q32.1-q32.2	SHGC-12033; D1S456-D1S2891
111	in Ovariumorgewebe überexprimiert	H.sapiens TROP-2 gene	thyroglobulin_1	1p32.2-p32.3	SHGC-12661; D1S476-D1S220
112	in Ovariumorgewebe überexprimiert	H.sapiens mRNA for Icn protein		11q14.1	SHGC-31540; D11S4179-D11S937;; SGC31540; D11D911-D11S1352
113	in Ovariumorgewebe überexprimiert	H.sapiens mRNA for BiP protein	HSP70; PRO_RICH	9q33.3-q34.11	WI-6005; D9S282-D9S260
114	in Ovariumorgewebe überexprimiert	H.sapiens HE4 mRNA for extracellular proteinase inhibitor homologue	wap	20q13.2-q13.13	SGC30446; D20S119-D20S197;; WI-30446
115	in Ovariumorgewebe überexprimiert	H.sapiens for neutrophil gelatinase associated lipocalin	lipocalin	9q34	
116	in Ovariumorgewebe überexprimiert	H. sapiens mRNA for Sm protein G		18q21.1	SHGC-8871 (D18S484;D18S851)
117	in Ovariumorgewebe überexprimiert	H. sapiens for glutathione peroxidase-GI	NLS_BP; GSHPx	14q24.1	
120	in Ovariumorgewebe überexprimiert	CDC28 protein kinase 2	CKS	9q21.31-q22.1	SHGC-11955; D9S1812-D9S283;; SGC31294; D9S153-D9S264
121	in Ovariumorgewebe überexprimiert	B-factor, properdin	VWA DOMAIN; TRYPsin_CATAL; sushi; trypsin		DXS255-DXS426
122	in Ovariumorgewebe überexprimiert	Annexin II	annexin	15q22.1-q22.31	WI-8600+WI-9161; D15S198-D15S159
123	in Ovariumorgewebe überexprimiert	ADP-ribosylation factor like 1	arf	12q22-q23.1	SHGC-12629; D12S1727-D12S78;; WI-7420; D12S346-D12S78
258	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 2			
259	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 3			

Seq. ID No.	Expression	Function
260	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 4
261	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 10
262	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 18
263	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 25
264	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 26
265	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 30
266	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 34
267	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 42
268	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 46
269	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 47
270	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 48
271	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 50
272	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 52
273	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 56

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Seq ID No.	Expression	Funktion	Module	Cylogenetische Lokalisation	nearest marker
260	in Ovartumorgewebe überexprimiert	Verlängerung zu Seq ID No: 4			
261	in Ovartumorgewebe überexprimiert	Verlängerung zu Seq ID No: 10			
262	in Ovartumorgewebe überexprimiert	Verlängerung zu Seq ID No: 18			
263	in Ovartumorgewebe überexprimiert	Verlängerung zu Seq ID No: 25			
264	in Ovartumorgewebe überexprimiert	Verlängerung zu Seq ID No: 26			
265	in Ovartumorgewebe überexprimiert	Verlängerung zu Seq ID No: 30			
266	in Ovartumorgewebe überexprimiert	Verlängerung zu Seq ID No: 34			
267	in Ovartumorgewebe überexprimiert	Verlängerung zu Seq ID No: 42			
268	in Ovartumorgewebe überexprimiert	Verlängerung zu Seq ID No: 46			
269	in Ovartumorgewebe überexprimiert	Verlängerung zu Seq ID No: 47			
270	in Ovartumorgewebe überexprimiert	Verlängerung zu Seq ID No: 48			
271	in Ovartumorgewebe überexprimiert	Verlängerung zu Seq ID No: 50			
272	in Ovartumorgewebe überexprimiert	Verlängerung zu Seq ID No: 52			
273	in Ovartumorgewebe überexprimiert	Verlängerung zu Seq ID No: 56			

TABLE II

Seq. ID. No.

ORF Seq. ID. No.

1	124	125	126	127	128	129
2	130	131				
3	132					
4	133	134				
5	135					
6	136	137				
7	138	139				
8	140	141				
9	142	143				
10	144	145				
12	148	149				
13	150	151	152	153		
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31	189	190	191			
32	192	193	194	195	196	
33	197	198	199			
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45	228	229	230	231	232	
46	233	234	235			
47	236	237	238			
48	239	240				
49	241	242				
50	243	244	245			
51	306	307				
52	246					
53	247	248	249			
54	250	251				

Seq. ID. No.

ORF Seq. ID. No.

55	252	253	254
56	255	256	
57	257		
258	274	275	
259	276	277	
260	278	279	
261	280	281	
262	282	283	
263	284	285	
264	286	287	
265	288	289	
266	290	291	
267	292	293	
268	294	295	
269	296	297	
270	298	299	
271	300	301	
272	302	303	
273	304	305	

The inventive nucleic acid sequences Seq. ID Nos. 1-123 and 258-273 of the determined candidate genes and the determined amino acid sequences Seq. ID Nos. 124-257 and 274-307 are described in the following sequence protocol.

Sequence Protocol**(1) GENERAL INFORMATION:****(i) APPLICANT**

- (A) NAME: metaGen - Gesellschaft für Genomforschung mbH
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1673
- (H) FAX: (030)-8413 1674

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Ovarian Tumor Tissue

(iii) Number of sequences: 284

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25 (EPO)

(2) INFORMATION ON SEQ ID NO. 1:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2434 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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cgggatttta cccgggttta aaagcgaacc ttctcccggc tacacccgaa ggtacccaaa 60
tatgggtagg tccgggtttt caacttggca aacgtatggg gaagcccggg gatggcttcc 120
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ttgcaaatat gcattttcaa acttgaaata taggtgtgaa cagtgtgtac cagtttaaa 240
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ttttaaatat tggacatact ggttttaata cctgctttgc atattcacac atggtcaact 360
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taaactagac atcttaattg gtgaaagttg tttaaactac ttattgttgg taggcacatc 720
gtgtcaagtg aagtagtttt ataggatagg gttttttctc ccccttcacc aggggtgggtg 780
gaataagttg atttggccaa tgtgtaatat ttaaactgtt ctgtaaaata agtgtctggc 840
catttgggtat gatttctgtg tgtgaaaggt cccaaaatca aaatggtaca tccataatca 900
gccaccattt aaccttctct tgttctaaaa caaaaaccaa agggcgctgg ttggtagggt 960
gaggtggggg agtattttta tttttggaat ttgggaagca gacagcttta ctttgaagg 1020
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(2) INFORMATION ON SEQ ID NO. 2:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 798 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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gcctatattg gaagcagaca gcgatactga tgacattgac cacagagtta cagaggaaaag 60
ccatgaagag ccagcattcc agaattttat gcaagaatcg atggcacaat actggaagag120
aaacaataaa taggagactt tagcacactt cacttgtttc tagaagtcca gaattttgga180
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cctcacactg tatagctcat tataggacgt cagggtttgtt gaaaaaagtg ggcaagacat720
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aaaaaaaaa aaaaaaaaaa                                     798
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(2) INFORMATION ON SEQ ID NO. 3:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 882 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

actgagtga gatgaaatca ggacactgaa acagaaaaaa attgatgaaa cttctgagca 60
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 tgaaggggcaa gatgaggaca ttttacctct aacccttgaa gagaaggaaa acaaagaata 180
 cctaaaaatct ctatttgaaa tcttgattct gatgggaaag caaaacatac ctctggatgg 240
 acatgaggct gatgaaatcc cagaaggtct ctttactcca gataactttc aggcactgct 300
 ggagtgtcgg ataaattctg gtgaagaggt tctgagaaaag cggtttgaga caacagcagt 360
 taacacgttg ttttgttcaa aaacacagca gaggcagatg ctagagatct gtgagagctg 420
 tattcgagaa gaaactctca gggaagtgag agactcacac ttcttttcca ttatcactga 480
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 tttggctgtg aaatttcaca ctatgataac tgagaagtgg ggattaaata tggagtattg 660
 tcgtggccag gcttacattg tctctagtgg attttcttcc aaaatgaaag ttgttgcttc 720
 tagactttta gagaaatata cccaagctat ctacacactc tgctcttctc gtgccttaaa 780
 tatgtgtgtg gcaaatcag tactgtttat gggagtatct gttgcattag gaacaattga 840
 ggaagttgt tcttttttcc atcgatcacc acaactgctt ttagaacttg acaacgtaat 900
 tgctgttctt ttccagaaca gtaaagaaag gggtaaagaa ctgaaggaaa tctgccattc 960
 tcagtggaca ggcaggcatg atgcttttga aatttttagt gaactcctgc aagcacttgt 1020
 tttatgttta gatggtataa atagtgcac aaatattaga tggataact atatagctgg 1080
 ccgagcattt gtactctgca gtgcagtgtc agattttgat ttcattgtta ctattgtgt 1140
 tcttaaaaat gtcctatctt ttacaagagc ctttgggaaa aacctccagg ggcaaacctc 1200
 tgatgtcttc ttgctggccg gtatcttgac tgcagtactg cattcactca acgaagtga 1260
 tggaaaatat tgaagtttat catgaatttt ggtttgagga agccacaaat ttggcaacca 1320
 aacttgatat tcaaatgaaa ctccctggga aattccgcag agctcaccag ggtaacct 1380
 aatctcagct aacctctgag agttactata aagaaacct aagtgtcca acagtggagc 1440
 acattattca ggaacttaaa gatataattc cagaacagca cctcaaagct cttaaatgct 1500

 tatctctggt accctcagtc atgggacaac tcaaatcaaa tacgtcggag gaacaccatg 1560
 ctgacatgta tagaagtga ttaccaatc ctgacacgct gtcagctgag cttcattgtt 1620
 ggagaatcaa atggaaacac agggggaaa atatatagct tccgtccacc atctatgaag 1680
 cctccacact gctgacatc aagtttttc ctaatgtgta tgcattgctg aaggtcctgt 1740
 gtattcttcc tgtgatgaag gttgagaatg agcggtatga aaatggacga aagcgtctta 1800
 aagcatattt gaggaacact ttgacagacc aaagggtcaag taacttggct ttgcttaaca 1860
 taaaatttga tataaaacac gacctggatt taatggtgga cacatatatt aaactctata 1920
 caagttaagt agagcttctt acagataatt ccgaaactgt ggaaaatacc taagagactt 1980
 ttaaaaatag gctttcttat atttgatatt tggaaagaaa agccgtaagg tgtatgtaga 2040
 ccacttaatc actaaatata tttgcctata ggactccatt gaatacatta gccattgata 2100
 atctacctgt ttaaatggcc cctgtttgaa ctctcaagct ttgaagacct acctgttctt 2160
 ccagaagaga acgttgaaa tgccatgttt ccttttgctg gatctctgtt gatggcactc 2220
 tggaaattgt tcagtttaagt catttttagac atagcattta ttatcactgt ggatctctac 2280
 ttgttgggtg ttatgaattc tttgaagaaa tatattttga agaggtgtgg gaggaaggaa 2340
 tacattttat aaaatgttgt agtgaagccc acaattgacc tttgactaat aggagttaa 2400
 agtatgttaa aaatctatac tggacagtta caagaaatta ccggagaaaa gcttgtgagc 2460
 tcaccaaaca aggatttcag tgtagatttt gtctttcttg aacttaaaga aacaaatgac 2520
 aaagtttgaa tggaaaagcc tgctgttgtt ccacatctcg ttgctgttta cattcctttg 2580
 tggagcctac atcttcttaa gctttttagc aggtatatgt tgaacacttc tgtttcatgg 2640
 ttgagacaga atcagaggcc atggatactg acaactgatt tgtctgtttt ttttctctgt 2700
 ctttttccat gactcttata tactgcctca tcttgattta taagcaaaac ctggaaaacc 2760
 taaaaataaa gtgtgtgtgt ttatctagaa aaatatggaa aatattgctg ttatttttgg 2820
 tgaagaaaaa caattttgta tagtttattt caatctaaat aaaatgtgaa ttttgtttaa 2880
 aaaaaaaaaa aaaaaaaaaa a 2901

(2) INFORMATION ON SEQ ID NO. 5:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 579 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

aaagaaagag aaagaaagaa aagaagattg tagctagggg gagagtaggt gaaaagatga 60
acaacatgac cgggaagatt tcctaattctc accacagcct ggctctacct taagtcttta120
ataaaagctt gactgaaggt accaaggtgt gctgaagtgg aagcaaagtt ctccaaagtc180
cagcatggta gacatcagtg gtggtaacca aggacagacc ccaaggcaag gtgaacctca240
aaaatggaac ctcaagtcta tgcagtccag ctgccctccc caccagaaag tccttggtcc300
agcccaacat cagtgcctct gagtttgttt actagaaaca aaggagaagt ttccttgtaa360

aaatatagac agagtagtcc ctggctttct cctcttgtag gaaggatgga ttctcccatt420
ccataccatc ttccccccac actggcccca gaaatactta attcaactat gtgaaaataa480
agattgtttt tggtttgagg gcatagggat ccatttatcc ttattcttta tgaggcacta540
aattagcttt gtatgttatt aaatgtgtct cgtcaatgc 579

```

(2) INFORMATION ON SEQ ID NO. 6:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2809 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

gcagggccctc	gtgcggtttg	cataaatag	ttttctcact	cttctttttt	tccttctttt	60
atccctcact	ccctcccta	aacctgtct	cagcacaaatg	gactaattct	agcattctga	120
tcataaggcc	ctccattttc	ctaattgtgt	tcaagggaatc	tttttaggaa	aaatatccag	180
attattcattc	cacttttttt	agtattctact	aaaaactcct	ttttttctct	agagagttat	240
gaaggaacag	gttgtccttg	tctggagtca	agctaaacac	atgatttgtt	ttatcgacag	300
ctggagcaga	agtgaaaaat	gtctttctgt	gagacagtaa	tttgctactg	aagctttatg	360
gcttggttgc	actgattact	ccaggatcca	aaaacttggt	gaaagtcact	gaaacactca	420
aggcaaatta	ctttacagcc	ctgagtgtct	gtcaccatag	tttgcataat	gaatatgaat	480
cccatttggtg	tgtgatgtag	gaaatcctgt	agttgtattt	tcttgaactg	aaatatgtga	540
ctcaaaaatac	ttaagactca	ttgtcatttt	tcactttggc	attattgtgg	acaagttgac	600
atattaaatac	tctttgtctt	ctggtaagct	tagcttttaa	aatgcatttt	cccttgtcct	660
gtctttcaact	agatatacat	gcttatattt	atagtgggtt	tcacagacta	taaaattgaa	720
tgtatgaaat	ttttattttat	atcagtgtct	ttaataaatga	agatattttt	ggagtaatgg	780
tgctgtcttg	tagcgagtta	ttaatcatag	taagattttt	ttctcttcag	ttgttttttt	840
tgtttcatat	taacaatttt	ttttttacac	ggacacaacc	ctctgcagct	ttcttcaaat	900
attaaaaatca	tttgaatatg	tatgctgtga	cttgaacact	gtctaacgcca	tcaagcagtc	960
ttcatacagt	ttgcattata	aaatctcatt	aaattctcca	agaaaaata	agttgaagaa	1020
ttttattttcc	tgaccatgca	tccctggat	ttctgagttt	cagttcagat	tgtagatgac	1080
aatataagct	gccttcogaa	attgtcaaca	tctgaatgtt	aagtcatttt	tccccatgg	1140
agaagcccg	agttccatga	agtagtgatt	accatttgtat	tttttctacta	acagtaaatg	1200
tatttttctt	attcaattgtt	tgctttagga	atgataaatt	acattttttg	ttcttcttal	1260
ccataaacat	ctgcattcct	cagctcagcc	ttccttgtat	gttggtttctt	tataaatggt	1320
tgagctgctg	atgcaggtat	tgccaagcta	acagtaaaaa	tcatttttaa	gaggaagctg	1380
gogcgatgg	cagccgagga	gcacactctg	caggacactg	gacaagacag	taaatattca	1440
acttttaaatg	ctgattaaag	gagtataggt	aaagaatacg	ttaggtataca	taattggtga	1500
gacaaatatt	cacttttatt	atattttata	tattattttt	ttattttggt	aaatactact	1560
cagttttgta	gttgctcctg	ttgatttgtg	tgatatttaa	gtatttagtaa	taattgccag	1620
gaaactatca	ttagggaggg	tttagttggt	tgctgtttgg	actgggaggg	atgattttaaa	1680
tttagtgcta	gaaaccaatt	tttagtgactg	cacagtttat	catttgtcag	acagaaggtat	1740
gctataaaag	taccctgtaa	gtcatatcaa	aaaagttcag	aggaagatta	gtaaatatttt	1800
atcaataaaa	taaacacattt	tgtttttcta	atattctaac	atattcctccc	ctttaggagg	1860
aagaacgtgc	aaaaacgtgag	gagctagagc	gaatactgga	agagaataac	cgaaaaattg	1920
cagaagcaca	agccaaactg	gccgaagaa	agttgagaat	tggtgaagaa	caaagaaaga	1980
ttcatgagga	aaggatgaaa	ctagaacaag	aacgacaacg	tcaacaaaaa	gaagacaaaa	2040
aaattatcct	gggcaagggg	aagctccaggc	caaaaactgtc	cttctcata	aaaaaccagg	2100
attaaattgc	aaactctgaa	cttttttcaa	agaaaaatgg	aaaaaacttg	tatggtagct	2160
tcatgttgaa	gtggtttttt	gtttttgttt	ttgttttttt	aatttgtaaa	atctggaaa	2220
ttagcttgtt	ctaatagggg	ctatgtctctg	caattccctt	tttttttttt	ttttttcctt	2280
ccactaagtc	aaatccttat	cagatcattg	ttgtatttcta	aggagtgcg	tatttttcac	2340
ctggtttgat	tctatatagg	tggtctgagg	aagagcagat	caacttgtaa	aactatggat	2400
ggtctgataa	ggcttttact	gcacccactg	acttcagagt	tatactctgt	ttgctacatc	2460
ataatgtctg	ttttgctgac	tttttggttt	tttatatatt	tataaaaaaa	gaaaaagttg	2520
gtgattgcat	tgggaaattc	ccagggtatt	actggacctt	tgtggtgtat	tgttaaacca	2580
gtgtccttgt	gatactgtgt	ctcttgatgt	tcttgataca	ggtaaggaaa	cagttggtca	2640
actctgatac	aaagtataata	tacagttcag	tattgtctct	gttcaatttg	tttttttttc	2700
attgacaaaa	tcaaacaggc	attccccatt	gtgtaaataa	atgattttgc	tgaataaagt	2760
aaaagctctaa	attcaaaaaa	aaaaaaaaaa	gaaaaaaaaa	aaaaaaaaaa		2809

(2) INFORMATION ON SEQ ID NO. 7:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 910 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

agttcggcac agagaaagta ttttaaccta cctgtagaga tcctcgtcac ggaaagggtgc 60
caaactgttt tgaatggaag gacaagtaag agtgaggcca cagttcccac cacacgaggg120
cttttgtatt gttctacttt ttcagccctt tactttctgg ctgaagcatc cccttggagt180
gccatgtata agttgggcta ttagagtcca tggaacatag aacaaccatg aatgagtggc240
atgatccgtg cttaatgata aagtgttact tatctaataa tcctctagaa agaaccctgt300
tagatcttgg tttgtgataa aaatataaag acagaagaca tgaggaaaaa caaaagggtt360
gaggaaatca ggcataatgac tttatactta acatcagatc ttttctataa tatcctacta420
ctttgggttt cctagctcca taccacacac ctaaacctgt attatgaatt acatattaca480
aagtcataaa tgtgccatat ggatatacag tacattctag ttggaatcgt ttactctgct540
agaatttagg tgtgagattt tttgtttccc aggtatagca ggcttatgtt tgggtggcatt600
aaattgggtt ctttaaaatg ctttgggtggc acttttgtaa acagattgct tctagattgt660
tacaaaccaa gcctaagaca catctgtgaa tacttagatt tgtagcttaa tcacattcta720

gacttctgag ttgaatgaca aagcagttga acaaaaatta tggcatttaa gaatttaaca780
tgtcttagct gtaaaaatga gaaagtgttg gttgggttta aaatctggta actccatgat840
gaaaaaagaa ttattttata cgtgttatgt ctctaataaa gtattcattt gataaaaaaa900
aaaaaaaaaa                                     910

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(2) INFORMATION ON SEQ ID NO. 8:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1447 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

gcgacggcgg cttagaaagt gcttctgga gcgcagacga ggtcatgaat catgtgacgg 60
tggtctgagg aggaacctgt ctttaaagct gtccctgaag tgacagcgga gagaaccagg 120
cagcccagaa accccaggcg tggagattga tcctgcgaga gaaggggggt catcatggcg 180
gatgacctaa agcgattctt gtataaaaag ttaccaagtg ttgaagggtt ccatgccatt 240
gttggtgcag atagagatgg agtacctgtt attaaagtgg caaatgacaa tgctccagag 300
catgctttgc gacctgggtt cttatccact ttgccccttg caacagacca aggaagcaaa 360
cttggaactt ccaaaaataa aagtatcatc tgttactata acacctacca ggtgggtcaa 420
tttaatcgtt tacctttggt ggtgagtttc atagccagca gcagtgccaa tacaggacta 480
attgtcagcc tagaaaagga acttgctcca ttgtttgaag aactgagaca agttgtggaa 540
gtttcttaat ctgacagtgg ttccagtgtg taccttatct tcattataac aacacaatat 600
caatccagca atcttttagac tacaataata cttttatcca tgtgtctcaag aaagggcccc 660
tttttccaac ttatactaaa gagctagcat atagatgtaa tttatagata gatcagttgc 720
tatattttct ggtgtagggt ctttcttatt tagtgagatc tagggatacc acagaaatgg 780
ttcagttctat cacagctccc atggagttag tctggtcacc agatatggat gagagattct 840
attcagtgga tcagaatcaa actggtacat tgatccactt gagccgttaa gtgctgcaa 900
ttgtacaata tgcccaggct tgcagaataa agccaacttt ttattgtgaa taataataag 960
gacatatatt tcttcagatt atgttttatt tctttgcatt gagtgaggaa cataaaatgg1020
cttggtaaaa gtaataaaat cagtacaatc actaactttc ctttgtacat attattttgc1080
agtatagatg aatattacta atcagtttga ttattctcag aggggtgctgc tctttaatga1140
aaatgaaaat tatagctaat gtttttcct caaactctgc tttctgtaac caatcagtt1200
tttaatgttt gtgtgttctt cataaaattt aaatacaatt cgttattctg tttccaatgt1260
tagtatgtat gtaaacatga tagtacagcc atttttttca tatgtgagta aaaataaaat1320
agtattttta aaaatataaa aaaaaaaaaa aaaaaataat tttttgttgc agactttttc1380
caaaaatcta aacataatta atatactctt tcagccacat gaataaataa tgagtgtttc1440
ttgtaaa
1447

```

(2) INFORMATION ON SEQ ID NO. 9:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 671 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```

agcgcgggtga agcggggggtg ggatctgaac atggcgggcgg tggtagctgc tacggcgctg 60
aagggccggg gggcgagaaa tgcccgcgtc ctccggggga ttctcgagg agccacagct120
aacaaggctt ctcataacag gaccggggcc ctgcaaagcc acagctcccc agagggcaag180
gaggaacctg aaccctatc ccggagctg gaatacattc ccagaaagag gggcaagaac240
cccatgaaag ctgtgggact ggcctgggcc atcggcttcc cttgtggtat cctcctcttc300
atcctcacca agcgggaagt ggacaaggac cgtgtgaagc agatgaaggc tcgggcagaac360
atgcggttgt ccaacacggg cgagtatgag agccagaggt tcagggtctc ctcccagagt420
gcccgcgtcc ctgatgttg gtctgggggtg cagacctgag gagcgctgcg accctcctag480
gctattgact gttaagtcc caggtttggc ccagattcca gttcgtgcct ctgaggtcca540
ccagagggcg catgaaagccc aggctgttgc caaacctac cctgccccac accaaggagc600
ccaccaaagg caaataaagt tattgagtgt ttagtagaaa ggaaaaaaaa aaaaaaaaaa660
aaaagtcgac c

```

671

(2) INFORMATION ON SEQ ID NO. 10:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 803 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:


```

gaagatgagg gaagaaga gtcaacagct ttgcaaaaaa ctcaaaaa ggaaattttg 60
aaaaaatcag agaaagatac aaatttctaaa gtaaaaccca aaggcaaaagt tcgatggact120
ggttctcggg cacgtggcag atggaaatat tccagcaatg atgaaagtga aggggtctggc180
actgaaaaat catctgcagc ttcagaagag gaggaagaaa aggaaagtga agaagccatc240
ctagcagatg atgatgaacc atgcaaaaaa tgtggccttc caaaccatcc tgagctaatt300
cttctgtgtg actcttgcca tagtggatac catactgcct gccttcgccc tctctgatg360
atcatcccag atggagaatg gttctgccc ccttgccaac ataaactgct ctgtgaaaaa420
ttagagggaac agttgcagga tttggatgtt gccttaaaga agaaagagcg tgccgaacga480
aqaagaagac gcttgggtgt tgttggtatc agtattgaaa acatcattcc tccacaagag540
ccagactttt ctgaagatca agaagaaaag aaaaaagatt caaaaaaatc caaagcaaac600
ttgcttgaaa ggaggtcaac aagaacaagg aaatgtataa gctacagatt tgatgagtt660
gatgaagcaa ttgatgaagc tattgaagat gacatcaaag aagccgatgg aggaggagt720
ggccgaggaa aagatatctc caccatcaca ggcatcgtg ggaaagacat ctctactatt780
ttggatgaaa aaataataac ggc
803

```

(2) INFORMATION ON SEQ ID NO. 12:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 828 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

agcacttcca ggctgggggtg tttgtttgga ctggagaagg gaggcggcgg gcgaaggcac 60
gtcgagcggg ggagcggcgc tgccgtgtga gatccgcgga ggccgacagg attcgttggc120
tgccgtcccc gctgctgtgc attgggttaa aaacgacaac caacatcagc catgaaagat180
ccaagtgcga gcagtactag cccaagcatc atcaatgaag atgtgattat taacggtcat240
tctcatgaag atgacaatcc atttgacagag tacatgtgga tggaaaatga agaagaattc300
aacagacaaa tagaagagga gttatgggaa gaagaattta ttgaacgctg tttccaagaa360
atgctggaag aggaagaaga gcatgaatgg tttattccag ctcgagatct cccacaaact420
atggacaaaa tccaagacca gtttaatgac cttgttatca gtgatggctc ttctctggaa480
gatcttgtgg tcaagagcaa tctgaatcca aatgc aaaagg agtttgttcc tgggggtgaag540

tacggaaata tttgagtga cggggccctc ttttggtgga tgtagcaca tttccacact600
gtgaaggcag tattagaaga ctttaattgta aaagctctct tgtcactgtg ttacacttat660
gcattgccaa agtttttggc agtcttgcac gcttaataaa agtgctgaga cacttgttac720
ctaagtaaaa agcctgtgac aaaccatttt actgggaaaa taggattggg gccccatggc780
cttggtgggt ggaagaccgc caaggggaag gaaccaccag gcccaagt
828

```

(2) INFORMATION ON SEQ ID NO. 13:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 552 base pairs
- (B) TYPE: Nucleic acid

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

ttggtttccg ggcgcaacca atgtgggagc tgtaatagta agagcttcct aaccaaagct 60
tggtattacc gtgtgggggt tcgttttttt cgtgggtggt tatttgattt tgattttttt120
ttcttttatg tgatcttttg gaaaacacat tcagaattat atctcgtttc tacttaaattg180
tagtgcttag ggtaattttt ttgtactgaa gtctttattg gtgggtgcat gctactggga240
acaagttttt gtacaaaagc ttcaatcaga atcactgtgc attactgaga ctctgtttat300
cactagcctt ctgtccctcc cgcagaagac tgttggttg aacaaaataa tatgtatttt360
gatttactta aagtgcctgt aaatttccta gggacctgcc acttttgact gtggatcagt420
tgatgtacac ttgtattatt aaagcactca ataaatcact gtggctgata actgcaaaaa480
tggaacccg acatttgctt tgtgtcctgg tgaccgtgt agccctacgt gcagtgaggc540
cttgtctaatt tc                                     552

```

(2) INFORMATION ON SEQ ID NO. 15:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 993 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```

gcgggtattaa tatttaattt atttttttta cttataggtc atgttgatgt ctatgataaa 60
cagatgtttt gcctctgaca gcagaacttc ctttcatttt tctcattcgt tttctttggt120
gggttcattt ttttgaatca accacacttc attattttcta ttaagcaatt tgacaggact180
gttgtagcct gcagtgtagt aaaccttctc atcgaaaact ttccatctt cccttaaaat240
gcttgctaatt gtcaaaagtt gttcttgatt cttttgggca ctagaaaatc catcgaaaaga300
ccgtacaaac acagtcattt cggctctatc ttcaatgaag acatctgact ctaaaggcct360
gggtggatca aattgctgtt cagagggaat atacaggga atggtaatgg tagactcact420
aaaaggacct gaaccaggct ccacgtagct tgtcactgga gctgtcatct ttattttcat480
ctctttctcg tttttgcctt gaatgtagct gttcagtttc gtaaagcccc tctggatggc540
tgaatcccag tccatagact ccacggacgt gctgaccac ttggctggtc catagtgtcg600
gatctcataa cttccgggct gggggccggc gtcctccgg gccttccagc ccggcgctctc660
cacagcttg ggcgcgcgt cctcgccgc cccggggtct ggctggagcg gctcggccat720
ggggcgcgctg acgctctggg agcctggtca gccgcgcaga ggccccgcac cccgggcccgc780
ccgcctgctg tgtgcgcgcc ccgcgaggg cccgagtcct cctccgcaga cccggtcctc840
cctcccggcc gggctggaga cccgagccca cccgatgcgt ctgcctctgg accgcgaggg900
ggcgccgcca ccaaggcggg gccggctcac gaccccgac agctccggc ggagttgcgc960
gtcctgcccc cgcccccccg cggcgacagg gag
993

```

(2) INFORMATION ON SEQ ID NO. 16:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2273 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```

ctgcacctta gaaaaaaaaa gaaaaaatcaa aaaaaacaaaa aaacaaaaaac aaaaaaagaa 60
ggaaaaatctt ggagggtggg cgtgggaact caggacccca gagtggcgag tgggtgggg 120
agggagagcc tctctccccc tttctgtgt gagagggaact cttagtgtct ggtgcagcta 180
ttaaattgtc aatgtgtcaa gtacgttgtt ttacacgcta caacatagct catttgaac 240
ccattgtata agctgtgtat ttacaaatat aacacaacaa ttttaactttt ccttagaata 300
caaaaaagtc tgcatggctt ggggaactat atgcttttcc atttttaagt. caggactgca 360
atactgattc cagttaatga gcagctaaga tccaatctgt ctaatacagt gaccccttag 420
ccatccgggc ctggcaatat acaatttttt tccccctcca agtttgaac actcccttc 480
cagaaaaggc ttgtgcaaca caggattatt tttaaatgat tctgaatttg aattaacttt 540
ttggagaatt ctgtgatgcc cttagaagaa attggacacg tattgagtgt cacaaagctg 600
gggctgggaa ttgtctgtct aatgtttcat tagacttaag aacctaaaat ttttctcagt 660
tgggtggata aaaccactaa cgcttagaaa ctgttttctc atgcagctat gtttctctta 720
tttatgcctt gaggactaat ttctgtgttt ctactgttta atgcactgtt gacctcata 780
atgggtgcctt acgcaagcga tccctctgtt ggggtgtctc tacaggggtg tgggcgatgc 840
atgctttatt aaggctcttg tttcacctgg cagtgtactg tatcaacgta taatacagaa 900
aaaaaatctc ttttaaggctc tcttcacaa agacatagag tgaaactccc tttacatgtr 960
agtatttgtt caacacttta ggcaacttga ctgtcagttg taaaaaggaa aacaggaaaa1020
tggaaaaatc tgaccaattc tgccaccttg agactttcat atagaccttg cacacaatt1080
gtatagatca cacaccggct gtatttaata tgaacattt tcacacatat taaagatacal1140
gaagtattaa aaaaccccca atgttaatgt atttgcttaa aaggcacaag tttcacatat1200
ctgtctagct atctgttggt aatacagaaa gtatactact tttttaaaaa agtgggcagal260
attcttgtgt atgtatatat gtgtgtacag tatgtgtatg tgtgtatata tatatattat1320
atatatagat aatatataaa tatttttttt aaggagaaac tagaatgttt agctagaaaa1380
ttccacagcc tgtgaagaaa tatttcaaaa tggccataaa ggaggtaaaa atgaaaaccal1440
taacctaaact tttatagagg ctttatcttt aatttaacga tgtgcggagg actttcttgc1500
ttgaatctgt tccgggctgt ctgctctgtc catcaaattg gcaggctctg aatggggcac1560
cttcggccgt tcagaagtgg cctgaacaga atgctggaac ccaggctgga ctcgacacal1620
ctaaggtttt gattttgaat ttcagcctta ttagaagatc taacctaaaga gtaagctaac1680
cacagggtatt cttttgtaga acacttttta tgcagatgaa gctatttttt ccagcaagtal1740
gattcttcca gtttttccaa ggagtaattt ccccgaattg gcataccacg gcgtggacag1800
ctgatatttc acccagctgc tggctgtgg gtgtggctct ttgctttata tatatatacal1860
cacatgtgag tctggctggg ctggtatttt gtttgatctt cctggaaaatg agcagtgact1920
aacgctcaca taactggttt tttttttatc tgggctgatg aatacattta cctaagaaac1980
tcatttcgtt ttacttaaga ggggaagtgc agttttcttt tggcagttca gaatccaagc2040
acttgatttg ctgggttttg aaaactcctt ttttggcctt ctatgtgctt agccataaca2100
attccattaa gcaagaaggt aagcaaaaaga caaaaaaaa aaagggaaaa aaaaaaaact2160
tgcaagggtc tgtctcactt acgaaacatg tcggagctgt ttgcctgggt ggggctgggt2220
accgtacctg tcaatgctg ggattttcca taaatttagc acgggacata aag 2273

```

(2) INFORMATION ON SEQ ID NO. 18:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 986 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

(2) INFORMATION ON SEQ ID NO. 19:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

gcgtctatat	tacatttatt	gacactggat	atttattatc	tggtatatac	caggcaaaaat	60
ggacacacca	tcaggagata	agacctgtat	cttacgtgta	agatgaaact	tatgcaaaaag	120
gcacagaaca	aattatttgt	tcacagttac	ttttaactct	ttcagcaatg	cctgagtcct	180
ctttatagaa	acttcatttt	gctaagttag	caaccattca	tttttttggt	tactcttcat	240
gtatagtatt	ctcaagtgtc	tcttcaaata	ctgcataatg	gtatagacca	tttaatatct	300
caaacataat	ctgaagaagc	agaggaatcg	ccatttaattt	catttgtgtt	tgacaaagcg	360
tcattccaatg	gattaaaaacc	cttcctttttg	gtggcagtg	aacggtatga	tacctaaaaa	420
gaaaaaaagag	ttaatcacct	ctcctggata	tgaatgctat	tagaagtttg	ttgactttct	480
ctaaattgat	aattgocctt	ctagatctat	aatgtagaga	gcaaaa		526

(2) INFORMATION ON SEQ ID NO. 20:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1765 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```

tttttttttt tttttttttt gctgtttttt atttattttg gattgttgtc aaataataat 60
ttttttttta aaaatctcaa aacatgttca aacacattca gtagcaaaga tccaccattg 120
gcacacacat taagaaagca cacacactag gcttctagtt gggctaatta aaatctctat 180
ggctggaaaag gtggttggtt gtacttaatt aagctttttt gaagtgcata gctatgcata 240
acagatgagc ttgaaagctg cagagtttaa gatagactta atttttcatg atttttccaa 300
agccagtcac gatattttatt taatttggtg tcttcagggt gcaccaatcc catgaagctc 360
aattggatac ttccactgct ttgtcaggta ttcatctgag aacttgacaa tgggtttttg 420
ccgaagatcg tagagaccaa gaggtttaag aagtcttgac acatctctcc agtctgcggt 480
tcttgctacc tcagctgaag gatacttctc cagaaacttc caaagcacag gtattgccat 540
tttgctgag gtccgattga gaaatatagt agcgatgaga agcttccatg gatcatgaaa 600
aagtgtttct tgaacgagat taaaagggtga ccgaggaggt gtccatttct taaaggcttt 660
acgtcggtgg gggctaagag cttctttgtt atatttgctg gaaaaatata ggcttggttt 720
ccttctttct atctgtgttc gtgggatggt atcttcagtg aagtctttcc tggttgggtg 780
gcagttgttg tccatttcag agccacgttt taaaatgtca gtatgcaaat gttctttcct 840
ttccacaact tctaactttt ttccgatttc ttcagattct aaaaagggtat cctcatactt 900
ctcgttgtgt tctgagtcct tggctgaaca aaatttggtt atgatgccag aagttttttg 960
ttcagaacaa aaatttgatc ctgaactcaa tgatctttct tttttttt caaggctgtt1020
ttcttctactg gtcacactga gggtctcacc acatgctcca gcatcagaaa tgcagacagt1080
tctatcaagc tgactttttt gtgcaacagg ttcactttca gcatctgctt tattacacac1140
agattctctt ttgctatcac ttgaaacaaa acctgaacag ctcttctac atcctttttt1200
agttttctta attgggattc ctttcaaaat agtcaccttt cctttgggct ttctaacctt1260
tctgaagtta acatcatcaa caccctcatc ttctttcaaa agcaaataag tggaaagtaa1320
gttagagagt cctctgctct cctgcaactc tgaactacta cttggcggtc taaacacatc1380
ctttttgcac ttgcttcggg tcttgaggtt ccagtttgaa ttgttacttt ggttttgtag1440
atgggatgtc agggctgcca tgctgcagtc tttatatctt gacttgatac cctttttag1500
aagtacagta aaatcaaaat cttctggctt aagagaagtc tctccatttt tgtgaagata1560
attagcaagt gaacttttgg atctgaactt cagtccttgt gggctagaaa atgatatta1620
aggaaactta ctgctagtaa atagaaggga cttttaaaag aactggacca catctcagat1680
ttctaattaa tttccaaatg ttgccatagg tatctgtcat ttaaaaatga aaaagagtga1740

```

1765

(2) INFORMATION ON SEQ ID NO. 21:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 746 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

gttttttttt gttttcttta aatttggatg tctctacacc actcctgatt tgtaggacta 60
aatagatcta tttattccaa tgcaaattgt gtaacattta tttcttccctt gatttttaaa120
aataacttttag tattctttaac tatgtatgtg ccttctctta cactgagttc ttttttgctc180
ctttcagctg ctcacacaat cctgtctgtt ggagtcatag ctgctaattc catattattt240
ctctacacac cttgaacatt tagtgtatta ctggtaccct tctgtgttct aggaaacaaa300
tgaattgcaa actggacttg taacaggatc atacatagag caacaaatta gctactggct360
ttgtaagata gtaagttagg aatttcacag tcatgtctcc aaatttcatg gcagagttta420
aaaaacaata taagactgtg gtaaggatca aacgcaaag caatttgctg tgactaattt480
cctaggactt atttcccttat gtaaaacccc tgttctttct ttctgcccac aagacagggt540
acaaagcttt ctaaaacatg ctctcagggtg tccacacctg agacattgct ttgtggatac600
tctcaaaggt gtccacaaag caaaaaaatc agaccaaatg ctaagagcaa gtaacttata660
cctcaccacc tggacatggc actggcaaaa gtcacttcag cattagaaca gtaatgtttt720
tgctaaatta ctaaaataat agccgc
746

```

(2) INFORMATION ON SEQ ID NO. 22:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 659 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

agcagactca caccagaact acattccctg gccccctgcc tgtgtgcttc tggccaggcc 60
ttggttggca agtctgacct gagaaaagga tctgcagaaa atcagactat gggatcactt120
tgtttgtgca ttgggaatga cattctttcc caccocagga aaacctttgg gactttcaga180
gacattgttg ctagccaacc acatgggtcag cctcaaagtt gagaggctca gtaaccttcc240
tatccctaga gaattccaaa gtgtggatgt aatttaacta gaaagccatt ggtgactatc300
tgtgatccct tggaaagtat ctatgtttgt tatatcttgc atccaaagcc agagggaaacc360
acaatgacta gtaaaacggt ggtctcaatg cccacttagc ctctgcctct gaatttgacc420
atagtggcgt tcagctgata gagcgggaag aagaaatatg cattttttat gaaaaataa480
atatccaaga gaagatgaaa ctaaatggag aaattgaaat acatctactg gaagaaaaga540
tccaattcct gaaaatgaag attgctgaga agcaaagaca aatttgtgtg acccagaaat600
tactgccagc caagagggtc ctggatgccg acctagctgt gctccaaatt cagttttca 659

```

(2) INFORMATION ON SEQ ID NO. 23:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 357 base pairs
- (B) TYPE: Nucleic acid

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```
cgcagtgcgc agccgtgggg ctctctcctt gtcagtcggc gccgcgtgcg ggctggtggc 60
tctgtggcag cggcgggcggc aggactccgg cactatgagc ggcttcagca ccgaggagcg120
cgccgcgccc ttctccctgg agtaccgagt cttcctcaaa aatgagaaag gacaatatat180
atctccattt catgatattc caatttatgc agataaggta aggcattcctt gtttttggac240
acagtctctt tactcagatc agctagtctt acatatgaat tttcttata gtcctcacaac300
aagtgcctaa aatgcctcgt tgtgctgtga gtaaagggtc gttgattagg ctggggcg 357
```

(2) INFORMATION ON SEQ ID NO. 24:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 890 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

cgagaggcagc ggaagccgca gccaggcgcc tgcgcgctgg gaagagtagg ttcaagagtgc 60
attccgggaac ccggggcgcg gcgcactgcg caggcgcccg gactccgctc agtttccgggt120
gcggcgcaaca ccaagtcgcg ggaacttaag cattttcggg ttctaggggtt gttacgaagc180
tgcaggagcg agatggaggt ggacgcaccg ggtgttgatg gtcgagatgg tctccgggag240
cgggcgaggct ttagcgaggg agggaggcag aacttcgatg tgaggccctca gtctggggca300
aatgggcttc ccaaacactc ctactggttg gacctctggc tttcatcct tttcgatgtg360
gtgggtgtttc tctttgtgta ttttttgcca tgacttggtc gctgatatct aaattaagaa420
gttgggttctt gagtgaattc tgaaaatggc tacaaacttc ttgaataaag aagacaggac480
tctcaataga agaatttcac atctccaagg gaccttctt ttcattttac actttgttac540
taatttgcag aactctatta attgggtagg atttcaccca ttcctagcta agttcttaaa600
attaaaccct ttgggttcgtg tttaaaaact ttcaaacatc tgatggcttt acaggggctg660
aatataaaag cttttgtact taaaggctct gtgtattcat taagaaatat agtaatgtct720
tttaaatgtt taagagttga tcagggttta ctatggatgg caagtaatag ggatgattaa780
taaggggaag gtttttatgg aatttcaaaa gtcaatttat ttcaaaagcg ggggaaaggg840
ttttgagagg agggggggccc aaggtgttcc tgggggttgc cgaggagggc 890

```

(2) INFORMATION ON SEQ ID NO. 25:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 651 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

gcccgtatatt gcatactaca tcagcaaaaag gtgttgccggc ttataaagcg ggcgctacgc 60
caccctcgagt cgtggtgcgt ccagagagac aaataccgat actttgcttg ttgatgaga120
gcccgggtttg aagaacataa gaatgaaaag gatatggcga aggccaccca gctgctgaag180
gagggccgagg aagaattctg gtaccgtcag catccacagc catacatctt cctgactct240
cctggggggca cctcctatga gagatacgat tgctacaagg tcccagaatg gtgcttagat300
gactggcctc cttctgagaa ggcaatgtat cctgattact ttgccaagag agaacagtgg360
aagaaaactgc gcagggaaaag ctgggaacga gaggttaagc agctgcagga ggaacgcca420
cctgggtggtc ctttaactga agctttgccc cctgcccga aggaaggta ttgccccca480
cctgtgtgtgt atattgtgac cagaccccg ggcggccca tgtagaaaga gagagacctc540
atcttctcatg cttgcaagtg aaatatgtta cagaacatgc acttgcccta ataaaaaatc600
agtgaatggg taaaaaaaaa agtgccattg tagtatgcaa taataagcgg c 651

```

(2) INFORMATION ON SEQ ID NO. 26:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1256 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

ctcgagccga attcggctcg agctttcctc tgaccatcca tatccaatgt tctcatttaa 60
acattaccca gcatcattgt ttataatcag aaactctggt ccttctgtct ggtggcactt 120
agagtctttt gtgccataat gcagcagtat ggagggagga ttttatggag aaatggggat 180
agtcttcatg accacaaata aataaaggaa aactaagctg cattgtgggt ttgaaaagg 240
ttattatact tcttaacaat tcttttttca gggacttttc tagctgtatg actgttactt 300

aaactatcta aaatagagca ttttggtatc tttcatctga ccatccatat ccaatgttct 360
catttaaaaca ttaccagca tcatgtttta taatcagaaa ctctggctct tctgtctggt 420
ggcatttaga gtcttttctg ccataatgca gcagtatgga gggaggattt tatggagaaa 480
tgaggatagt ctctcatgac acaataaata aaaggaaaaa taagctgcat tgtgggtttt 540
gaaaaaggtta ctatacttct taacaattct ttttttcagg gacttttcta gctgtatgac 600
tgttacttga ccttctttga aaagcattcc caaaatgctc tatttttagat agattaacat 660
taaccaacat aatttttttt agatcgagtc agcataaatt tctaagtcag cctctagtcg 720
tggttcacat ctttcacctg cattttatct ggtgtttgtc tgaagaagg aaagaggaaa 780
gcaaatagca attgtactat ttgtaccaaa tctttgggat tcattggcaa ataatttcag 840
tgtgtgtgat tattaaatag aaaaaaaaaa tttgttttcc taggttgaag gtctaattga 900
tacgtttgac ttatgatgac catttatgca ctttcaaatg aatttgcttt caaaataaat 960
gaagagcagc tgctcttctt tctcttttta agtggtcagc tgtggcatgc tcagaggttc 1020
ctgttggtat ccagctggag cgggtgtgata ccttctttt tcagctgttc gtgccttctt 1080
tttttgatc caccaaagtg gagacaaata catgatctca aagatacaca gtacctactt 1140
aattccagct gatgggagac caaagaattt gcaagtggat ggtttggtat cactgtaaat 1200
aaaaagaggg cctgggaatt cttgcgattc catctctaaa aaaaaaaaaa aaaaaa 1256

```

(2) INFORMATION ON SEQ ID NO. 27:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 694 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

gtttctaaag gatgtgtaag aaaccagagg taaagggtctc gcgatatctt aagacatccg 60
gcgtagtacg cttcagtgag ccacagcgct agagaagtag gagaagctcg cgagatctgt120
gccgttgccg aggagactag gagggggagg agaggggatc tcgCGaaagg aaagaggtcg180
ggagcgctcg cgagatctcg gaccacccaa cctgaaagggt gcttaggaag ttgaaaggcc240
cagaggaggc ctccgggcaa atggccggag ctggaccgac catgctgcta cgagaagaga300
atggctgttg cagtcggcgt cagagcagct ccagtgtctgg ggattcggac ggagagcgcg360
aggactcggc ggctgagcgc gcccgcagc agctagaggc gctgctcaac aagactatgc420
gcattcgcat gacagatgga cggacactgg tcggctgctt cctctgcact gaccgtgact480
gcaatgtcat cctgggctcg gcgcaggagt tcctcaagcc gtccgattcc ttctctgccg540
gggagccccg tgtgtggggc ctggccatgg taccgggaca ccacatcggt tccattgagg600
tgcagagggg gagtctgacc gggcctccgt atctctgacc acgatggcgc ttacctttca660
gacttcatta aacttatgac cgaaaaaaaa aaaa

```

694

(2) INFORMATION ON SEQ ID NO. 28:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1927 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```

gagagatattt attttttttt tttttttttt acagaaattg acctttattt gttgtactaa 60
agcctgttta acttttgata caaagtaaca ttttagtaca gaaaatccca gtctgtcagc 120
ttagtacctg tctgtgcaca ctgtaccatc tcagtccac tctgctgtta acttagaaaa 180
cagcccttac ccccagaggg tctgagagtt aataccttga gaatagtcta cagtttttca 240
tagtttgtct gagctagaaa acttgtacct gtaaaacaaa ggacagcatt gaggactgaa 300
acttgtctct tttttgaaca actgtgcaag aaaatatatc cttttttaaa aaacatcagt 360
tatggctaaa ctacaatcta gtgtctagaa ttacaaagaa taaaatgaaa tcaaagattt 420
ctcgctagta aaatgaaatg ttaggaacag tattaataaata taggtcctac cccaacgaca 480
cttacacaga gccagtaga gtacctatta ttaacaggac gcatagctta aggaggaacc 540
acatcaaata ttcagccaga catatctagc ctacagaagt caaaaaaaaa aaaagccccc 600
aaacgaagac acccacactg agtaggggtg atgccgtgag tgctgtaatc aagattaaaa 660
agacctcagt ttttcttttt agactgttga tagtgacaat aaccattatg cttcccttaa 720
aagctctcaa ttaaatgtct gaaacatgaa tgttttcata tcaaaaagaa ctgatgtacc 780
tgccaccctc taaaaagttt aagaattacc ctgcaaacat tgcaactgat aaggctgtca 840
cgacttacag agcctaagga ggacccaatg gcaggcatca gcacagctga acaccacctg 900
gaccccaactg cagccctgcc cacgcagctc tcacggagca gacacagtcc tcaagtaata 960
agcacagatg gaggagaaac gagaggctgt ggaaggcagg agagaaaggc cgagagacga 1020
gtttgttaaga atgccaagt cacttcccc attgtgggag gaaaatgcca aaggcactgg 1080
ttctgtctgc acaggcagtc tgagcacctg gagttgtgac gtccctccag gagagggtgc 1140
accaaggagc aggaggtttg tcaaagctct ggtcccacca acaagaacct cccaaagcaa 1200
agcagcccc attgaggttc caaggtcgtt ttgctgaaga cgggaacgaa accaacacca 1260
aagcgacagg ggggtgacag aggggacagg ggctgggcac cggcaacatg gagccgttca 1320
agtaaacata aaccacaaaa tacttagaaa aggcttgtaa acgagtgatc cgaaaggttc 1380
tctttgcagc atctctgatc agctggctaa agaaagggtg gtgctgaacc cgtctttagt 1440
gttatctgtt ttgtgttaaa gcacacgtgt gacacgggca gagtgtgtgg gcctgggcct 1500
ggatcgcacg cagccgtggc cctctgtcta caaaggaggt gcttctgggt cctgggtccg 1560
gatccttccc ccgcatgttc atagacggac agacttctac tttcagtcgc tagaaaagag 1620
ctgagctctg tgctccctca ggcggccagc tgcagtcac cacagcacag cattctccta 1680
gagcgggcag gctggaatcc acaggacttt atttgttct tgattgacca ttgccaagat 1740
ctgagtgcaa atgcttgaca gggctcctcc ctggatgacc cctgcaaaa agccccccag 1800
acacgtcatt cagctcagag taagacccca gggttgaggc aaggcagtag agcttgcaat 1860
ctttctactg tgtggctgtc tgctttgtgc tccttggcac tctgtccat cccacctga 1920
ctctcct

```

(2) INFORMATION ON SEQ ID NO. 29:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 672 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```
gcctttttat tttttttttt tggtcgttat gctgcattta ttatgagaat caacagtcaa 60
cagttaatga ttgactaact cttgttggtc actctggaca ttaacgaaaa agactggaat120
agggctacag cgctgctttt atgctacacg gggtatgctt ggactctgac tcccagcagc180
aggtagattc aggaattcat ggcagtgcac ttcaccatca tgggaaacac cttccctttt240
cttcaggatt ctctgtagtg gaagagagca cccagtgttg ggctgaaaac atctgaaagt300
agggagaaga acctaaaata atcagtatct cagaggggtc taagggtgcc aagaagtctca360
ctggacattt aagtgccaac aaaggcatac ttctggaatc gccaaagtcaa aactttctaa420
cttctgtctc tctcagagac aagtgcagct caagagtcta ctgctttagt ggcaactaca480
gaaaactggt gttacccaga aaaacaggag caattagaaa tggttccaat atttcaaagc540
tcgcacaaca ggatgtgctt tcctttgccc atttagggtt tcttctcttt cctttctctt600
tgtttagtct tcgttctctt tttcagttc catcagatct cccctcgtg ccactggaat660
ctcagaggtt gc                                     672
```

(2) INFORMATION ON SEQ ID NO. 30:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 269 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

ccgcataccta gccgcgcgact cacacaaggc aggtgggtga ggaaatccag agttgccatg 60
gagaaaaattc cagtgtcagc attcttgccg cttgtggcgc tctctacaa tctggccagg 120
gatagcacag tcaaacctgg agccaaaaag gacaggaagg agtctcgagc caaactgcgc 180
cagaccctct ccagaagttg gggtgaacaa ctcatctgga ctgagacgta tgaagaagct 240
ctatataaat cgagactagc aactaacc 269

```

(2) INFORMATION ON SEQ ID NO. 31:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 604 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual
 ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

tgcgagggcg ggatagctgt ccaaggtctc cccagcact gaggagctcg cctgctgcc 60
tcttgccgcg ggaagcagc accaagttca cggccaacgc cttggcacta gggccagaa 120
tggctacaac agtccctgat ggttgccgca atggcctgaa atccaagtac tacagacttt 180
gtgataaggc tgaagcttgg ggcacgtcc tagaaacggt ggccacagcc ggggttgta 240
cctcggtggc cttcatgctc actctcccg tctctgctg caaggtgcag gactccaaca 300
ggcgaaaaat gctgcctact cagtttctct tctctctgg tgtgttggc atctttggc 360
tcaccttcgc cttcatcctc ggactggacg ggagcacagg gccacacgc ttcttcctct 420
ttgggatcct cttttccatc tgcttctcct gcctgctggc tcatgctgtc agtctgacca 480
agctcgctcg ggggaggaag cccctttccc ggttggtgat tctgggtctg gccgtgggct 540
tcagcctagt ccaggatgtt atcgctattg aatatattgt cctgacgatg aataggacca 600
aggt 604

```

(2) INFORMATION ON SEQ ID NO. 32:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 781 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

ctttaatgtg cctagagcaa tggaatgggg cactttgggg gcggtggaat tcaagacgct 60
ctggctgaag attcagaagt atctggtaac tctcttttcc ttctgggcat cctctcctct120
gttctaatac tcccttacac tcattcctgg tccattgtat tctgaccaca tccctaatac180
tggtcaaaaa tattgagtcg tgggcacatt ggatcatgaag gaacaagaag gcaatgagag240
actctcatgc caaccactgc cctgaaagcc ctgctgttca gacagcaaag gggccagcac300
tggccaagct cttatgcttg ctctgaaacc ttcttgggag gactcaatag ggtctccttt360
tgaaagtgtc cctggccttt tgagaaagca gtgtgggtga gggagatggt tctggcaggga420
gocgtgaatg gttgttttct acttgggatt tcttctctgc tttaggagat ctattgggaa480
actgattata accactcggg caccatcgat gcccacgaga tgaggacagc cctcaggaag540
gcaggtttca cctcaacag ccaggtgcag cagaccattg ccctgcggtg tgctgcagc600
aagcttggca tcaactttga cagcttcctg gcttgtatga tccgcctgga gacctcttc660
aaactattca gccttctgga cgaagacaag gatggcatgg ttcagctctc tctggccgag720
tgctgtgct gcgtgttggt ctgaccgcc aaacttgacc tagaagatgg ggggggcctc780
c
781

```

(2) INFORMATION ON SEQ ID NO. 33:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 304 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```

ggccactgcg gcgagacgcg aggaactgtc gctcgtactc gtgcgcctcg ctttgctttt 60
cctccgcaac catgtctgac aaacccgata tggctgagat cgagaaattc gataagtcgal20
aactgaagaa gacagagacg caagagaaaa atccactgcc ttccaaagaa acgattgaac160
aggagaagca agcaggcgaa tcgtaaggag gcgtgcgccc ccaagtatgc actgagatgc240
gagaagtgtt gcgtcgaatt tacctgcttg agggggtaaa gttgggaagg tggaaaagg300
gtgg                                     304

```

(2) INFORMATION ON SEQ ID NO. 34:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1528 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```

aattcggatc catgggccac agtggatggc ttgaaatgtg gctgagcgct tcggacactt 60
cggatccatg gtggccaccc caagacgcgc cccagcccgc catggcccgg atcctccggg 120
atcctgcctt ctgtccctgc tcctggccgg gtttgttccg ccgggcccgg gacaagagaa 180
gtctaagaca gactgccatg gcggtatgag tggtagcatc tacgagtatg gagccctcac 240
catcgatggg gaggaataca ttcccttttaa gcagtatgca ggcaaatata tcctctttgt 300
caacgtagcc agctactgag gtctgacaga ccaatacctt gaactgaatg cactacaaga 360
agaacttggg ccatttggct tggtcattct gggcttccct tccaaccaat ttggcaaaaca 420
ggagccaggc gagaactcgg agatactccc cagtctcaag tatgttcgac caggtggggg 480
ctttgtgcct aatttccagc tctttgagaa aggagatgtg aacggggaga aagagcagaa 540
attctacact ttctgaaga actcctgccc tcccactgca gaactcctgg gctcacctgg 600
ccgcctcttt tgggaaccca tgaagatcca tgacatccgc tggaaacttg agaagttcct 660
ggtggggcca gatggcatac cggttatgag ctgggtaccac cggaccacag tcagcaacgt 720
caagatggac atcctgtctt acatgaggcg gcaggcagcc ctgagcgcca gggggagta 780
actgatgccc ccaccctacc cctacccctt gcccatcatg caagggccga ggaggggctc 840
ttcaggaagg aagccacatt cccagtcatt ctacccccac cccagattct ctttcttatt 900
acataaaaga caagcctggc acaactgtgt gtctgaacca ctgtggacac gtgacaattg 960

```

(2) INFORMATION ON SEQ ID NO. 35:

(A) LENGTH: 499 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ggcagggtctc	agcgctctctc	cccctgctcc	gtctctctgc	agggccagg	cgcccttggc	60
cttaggaccc	aacttctctt	accgccatgg	agttcgacct	gggagcagcc	ctggagccca	120
ctctccagaa	gcccggtgtg	ggggcgggcc	acgggggaga	tcccaagctc	agtccccaca	180
aaagttaggg	ccggtcggag	gcaggggcag	gtccgggtcc	aaagcaagga	caccacagct	240
cttcgactc	cagcagcagc	tccagcgatt	cggacacgga	tgtgaagtcc	cacgctgactg	300
gtccaagca	gcacgagagc	atcccgggca	aggccaagaa	gcccaaatgt	aagaagaagg	360
agaagggcaa	gaaggagaag	ggcaagaaga	aggaggctcc	ccactgaagg	cgcttgacaa	420
gggtcatta	aaccttctc	tctgcctacg	agtaccaacc	acctggagct	aagatgctta	480
ggtggggggg	ggcgcgca					499

(2) INFORMATION ON SEQ ID NO. 36:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1396 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

gggcacccgt tagttgggaa cagcggaaacg ctggtcccg ggactgagta aggtgtctgg 60
atcggaggga ggttcgggtg ggcacgggc ggctggaaga gctcgactcg tcccgtctgg 120
aaagcgcgag tctgagtggg accctggacg acttgacag cggctggcgc agtcattggc 180
gactactgga agtcacagcc aaagaaattc tgtgattact gcaagtgtcg gatagcagac 240
aataggccta gtgttgaatt tcatgaaaga ggaaagaatc ataaggaaaa tgtggcaaaa 300
aggatcagtg agattaaaca gaaaagcctg gataaggcaa aggaagaaga aaaggcatca 360
aaggagtttg ctgcaatgga ggcagctgcc ctgaaagcat accaagagga tttgaaaaga 420
cttggcttag agtcagaaat tttggagcca agcataacac cagtaaccag cactatccca 480
cctacctcga catcaaatac acagaaagaa aagaaagaga agaagaaaaa aagatccttc 540
aaagggcaga tgggtagaag gcataacctc tgagggttac cattactatt atgatcttat 600
ctcaggagca tctcagtggg agaaacctga aggatttcaa ggagacttaa aaaagacagc 660
agtgaagacc gtttgggtag aaggtttaag tgaagatggg tttacctatt actataatac 720
agaaacagga gaatccagat gggagaaaacc tgatgatttc attccacaca ctagtgatct 780
gccttctagt aaggtcaatg aaaattcact tggcacccta gatgaatcca aatcatcaga 840
ttcgcatagt gattctgatg gggaacagga agcagaagaa ggaggggtct ctacagagac 900
agaaaagcca aaaataaagt ttaaggaaaa aaataaaaaat agtgatggag gaagtgaccc 960
agaaacacag aaagaaaaaa gtattcagaa acagaattca ttaggttcaa atgaagaaaa 1020
atcgaaaact cttaagaaat caaacccata tggagaatgg caagaaatta aacaagaggt 1080
tgagtctcat gaggaggtag atttggaact tccaagcact gaaaatgagt atgtatcaac 1140
ttcagaagct gatggtggcg gagaacccaa agtggtatct aaagaaaaaa cagtcacttc 1200
tcttggagtt atggcagatg gagtggcccc agtcttcaaa aagagaagaa cttgaaaatg 1260
ggaaaatctt aggaaaattt aagggcaacg aggtgatgat ccaatagttt gcagggagag 1320
ctttttgtt acatgctttt tagggaccag aatggggaga ctttttgcca cccccaaggt 1380
ttgtcccggt ttttgt

```

1396

(2) INFORMATION ON SEQ ID NO. 38:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 808 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

cctctgtcca ctgctttcgt gaagacaaga tgaagttcac aattgtcttt gctggacttc 60
ttggagtcct tctagctcct gccctagcta actataatat caacgtcaat gatgacaaca120
acaatgctgg aagtggggcag cagtcagtga gtgtcaacaa tgaacacaat gtggccaatg180
ttgacaataa caacgggatgg gactcctgga attccatctg ggattatgga aatggccttg240
ctgcaaccag actcttttcaa aagaagacat gcattgtgca caaaatgaac aaggaagtca300
tgccctccat tcaatccctt gatgcactgg tcaaggaaaa gaagcttcag ggtaagggac360
caggaggacc acctcccaag ggctgatgt actcagtcaa cccaaacaaa gtcgatgacc420
tgagcaagtt cggaaaaaac attgcaaaaca tgtgtcgtgg gattccaaca tacatggctg480
aggagatgca agaggcaagc ctgttttttt actcaggaac gtgctacacg accagtgtac540
tatggattgt ggacattttc ttctgtggag acacgggtgga gaactaaaca attttttaaa600
gccactatgg atttagtcat ctgaatatgc tgtgcagaaa aaatatgggc tccagtgggt660
tttaccatgt cattctgaaa tttttctcta ctagttatgt ttgatttctt taagtttcaa720
taaaatcatt tagcattgaa acggagaact ctgcgggcta gtaaccacaa ggtacggagc780
aaagatcacc caggtgggaa gaggtgga                                     808

```

(2) INFORMATION ON SEQ ID NO. 39:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1139 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```

tttttttttt tttttttttt tttttttgcag caatacctcc tttatttgat ccctgtttat 60
gtccacatat gtactgtatt atcacagatg caactgattt atcatagagc actcagaaaa 120
catggaaaaa tatttttaaa aatcgaataa tcctattcaa gtcaaccagt gttaaccccc 180
gtgtgcttcc tgccagtcctg ttccctcccca tgggagtcac acaaaatgaa aatctcctag 240
aaagagaaat tcctctgtcc tctgacttct tcacttagta cgctgcgacc ttcccatgtt 300
gttcaacatc ctcaactcgg agcgtcactg gctggagggtg gtctataaat ggaattggct 360

taactatctc ttcactgaaa ggtggacatt tagggagtggt ccagttttca gctgtcataa 420
acaactgcct tagacggcaa agaattcaca ggtcaatcgt tcccttcgct ttgaacttct 480
tcgcagaccg ttcacttgac cgaagctgga atttgctccc gtaaatgtag gaaataaaagc 540
cctcggtttc cacagtgaac acgcagttta gcttggggat aactttcagg cggctcttct 600
tggtgataat tttgaaaatg tgctttgttt cctgtagaag gattcctgta ataccacat 660
aagaggggca tttggatttt gtcactgaaa taatagcccc gtgaagatct gcctttaaga 720
gcttggcctg aatcatctgt ggctgcgtgt ctggcttgag cccactgcac aggtccctga 780
tgtactgttt ccagagttca tggagaggga ggaaaaggct gtatctctgc tgcctctggt 840
taatgtcaaa gagccgcagc tccctccttt gcctggcaga gaagcctttg gctttcttct 900
tcttctcctt gcgcttggtg cgggtgaagt actccaggac caccgccttg cgctgcagct 960
ggctcctcgg ggccctgcgg ctcatgcggg gcgtctgcgc ttcaggaagg ccttcacgaal1020
ggcctcggcc cgctgtgctc ctgaaggctg gacatcgag tcattcgctt cttctgaga1080
caatgcattg tagatcacac tcttcattct cggaccgctt ccggcgctct ctgatgacg 1139

```

(2) INFORMATION ON SEQ ID NO. 40:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2177 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

gccccagcgt cccgtcgccg ccggcagcga acagcagcag cagtcagcct tcattcagga 60
aagacagcca gttgctctca tgcgtttatt gtctttcaat gtgcctcata ttaaaaaacag 120
cacaggagaa ccaatatgga aggtactcat ttatgacaga tttggccaag atataatctc 180
tcctctgcta tctgtgaagg agctaagaga catgggaatc actctgcac tcgttttaca 240
ctctgatcga gatcctattc cagatgttcc tgcagtatac tttgtaatgc caactgaaga 300
aaatattgac agaattgtgc aggatcttcg aaatcaacta tatgaatcat attattttaa 360
ttttatttct gctattttcaa gaagtaaaact ggaagatatt gcaaatgcag cgtttagcagc 420
tagtgagta acacaagtag ccaaggtttt tgaccaatat ctcaatttta ttactttgga 480
agatgatatg tttgtattat gtaatcaaaa taaggagctt gtttcatatc gtgccattaa 540
caggccagat atcacagaca cggaaatgga aactgttatg gacactatag ttgacagcct 600
cttctgcttt tttgttactc tgggtgctgt tcctataatc agatgttcaa gaggaacagc 660
agcagaaaatg gtagcagtga aactagacaa gaaacttcga gaaaatctaa gagatgcaag 720
aaacagtcct tttacaggtg atacacttgg agctggccaa ttcagcttcc agaggccctt 780
aattgctcct gttgacagaa acatagattt ggcaactcct ttacatcata cttggacata 840
tcaagcattg gtgcacgatg tactggattt ccattttaa acagggttaatt tggagaagatc 900
ttcaggagtg gaaaactctc cagctgggtgc tagaccaaa agaaaaaaca agaagtctta 960
tgatttaact ccggttgata aattttggca aaaacataaa ggaagtccat tcccagaagt 1020
tgcagaatca gttcagcaag aactagaatc ttacagagca caggaagatg aggtcaaacg 1080

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acttaaaagc attatgggac tagaagggga agatgaagga gccataagta tgctttctga 1140
caataccgct aagctaacat cagctgttag ttctttgcca gaactccttg agaaaaaaag 1200
acttattgat ctccatacaa atgttgccac tgctgtttta gaacatataa aggcaagaaa 1260
attggatgta tattttgaat atgaagaaaa aataatgagc aaaactactc tggataaaatc 1320
tcctctagat ataataatcag accctgatgc aggaactcca gaagataaaa tgagggtgtt 1380
tccttatctat tatataagca cacagcaagc accttctgag gctgatttgg agcaatataa 1440
aaaagcttta actgatgcag gatgcaacct taatccttta caatatatca aacagtggaa 1500
ggcttttacc aagatggcct cagctccggc cagctatggc agcactacca ctaaaaccaat 1560
gggtctttta tcacgagtca tgaatacagg atcacagt ttgtatggaag gagtgaagaa 1620
cctgggtttg aaacagcaaaa atctacctgt tactcgtatt ttggacaatc ttatggagat 1680
gaagtcaaac cccgaaaact atgactatag atattttgat cccaaaatgc tgcggggcaa 1740
tgacagctca gttcccagaa ataaaaatcc attccaagag gccattgttt ttgtgggtgg 1800
aggaggcaac tacattgaat atcagaatct tgttgactac ataaagggga aacaaggcaa 1860
acacatttta tatggctgca gtgagctttt taatgctaca cagttcataa aacagtgtct 1920
acaacttggg caaaaagtaac acagaagaac cttactatga taatctactt ggaatgtgga 1980
taaatgtaaa aagaagaaaa gttagaagag caatatgttt ccttctctgt aacagtgtcc 2040
taacagtgaa aatcagagtt atttgttaat ttttaaggaa attatatact taatatgtat 2100
tgatttaaaag aaacatttca gaaataaaat ttcaacattg taaaaaaa gtcggctacc 2160
tacacggata atatcgc
2177

```

(2) INFORMATION ON SEQ ID NO. 41:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 402 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

ggcgccaggcc ccagccagct caggctacac tatcccagga tcagcatggc cgtccgccag 60
tgggtaatcg ccctggcctt ggctgccctc cttgttggtg acaggggaagt gccagtggca120
gcaggaaaagc tccctttctc aagaatgcc atctgtgaac acatggtaga gtctccaacc180
tggtcccaga tgtccaacct ggtctgcggc actgatgggc tcacatatac gaatgaatgc240
cagctctgct tggcccggat aaaaaccaa caggacatcc agatcatgaa agatggcaaa300
tgctgatccc acaggagcac ctcaagccat gaagtgtcag ctggagaaca gtggtgggca360
tggagaggat atgacatgaa ataaaagatc cagcccaact ga 402

```

(2) INFORMATION ON SEQ ID NO. 42:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1349 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```

cttcttttgc catcccatct ccttggcact gcaccatttc cccaattatt ggccaatccc 60
taggctttct gggttttaca atggttgcga ccacaatcag gctcatagat ggctccaatt 120
taaaaaaaaaa ggtaatgggt atggataaaa taagcagatc aagggaagtg tgctatcata 180
aaataactgt agcttcaaca tcttgagtac cagtttcctg gcagatagta aacatccaat 240
cacaagggat ttttctgaa ggggtgtaaag ctggtttgaa aattcttcag tcacagagca 300
gcctacacat gccaattaga aactgacaga cactagatgt gcttgggaaga ttaaacacta 360
cgtacagaaa cagcagttac taagctcctc agtagtttct tgtctttttt aagtttcgct 420
gaatcgacag tttgcacaac gtgctatatt ctgtgggtca aaaccaagta aatactgtgt 480
aaagttggca gattttttcca gctaagatca agaaaaaaca aattttctga taaaacaggt 540
ttagagtcag aaacactctc taaagtcaa aactgatggt ccacgatctc aaatagctaa 600
aactcctgca gaatggaagg gagagacgtg aaacagggaa ataaattaca gtcagtgtgt 660
gttaatttag gaaaagggaa aaataaacca aactcaagtc ggtaaagtgt atcaaaaat 720
tcaatgatgt agctttcccc actctctgtc acacacgctt gctaacaagt atattaaatt 780
aaggccaaat ttaacctgaa tgcgtttttt tttttctttt tattaagatc tgagatagga 840
acggtcatac ttagtactga aaggcagaca ataaaatggg ccatgaaagg ggggggaaag 900
gtactgtcta ttgttcgagg gattcaacca gagataaaac ctatatacaa gcatgtgtgt 960
agctcgaaat aaaaataaaa ggactatttc atgtcatgac tgcttggttg cttcctcttcl 1020
atatgcattc cctgtgccat tctgtacata ggatgaacca gaaccaaggc catacaaatg 1080
accacaatat ttggcatcat caatatgatc ttcaaagaac atttctctca ttttgaaaaa 1140
ggccattcct gtgagcaatg aatcagatcc tgctgatgt tgtgggtccta tccgttccag 1200
ctctaactgt tctgccacct cctgtaatcc acctttgaga tttttcctgt catttatgat 1260
gtgaagtacc tcatgaagag ctgcaaaaat ctctaactgt tctgccacct cctgtaattg 1320
cgagtcagtg attgacgaaa taatagtcg 1349

```

(2) INFORMATION ON SEQ ID NO. 43:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 3552 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```

atttaattctt cattcttcta ctatccccc aa tccctaatttc aatatcaaac ctaattaaac 60
acatcaactt cccactgtac accaccacat caatcaaatt ctcccttcatt attagcctct 120
tacccttatt aatatttttt cacaataata tagaatatat aattacaacc tggcactgag 180
tcaccataaa ttcaatagaa cttaaaaataa gcttcaaaac tgactttttc tctatcctgt 240
ttacatctgt agcccttttt gtcacatgat caattatata attctcttca tgatatatac 300
actcagaccc aaacatcaat cgattcatta aatatcttac actattcctg attaccatgc 360
ttatccctcac ctccagccaac aacatatttc aacttttcat tggctgagaa ggggtgggaa 420
ttatatcttt cctactaatt ggatgatggg acggacgaac agacgcaaat actgcagccc 480
tacaagcaat cctctataac cgcacgggag acatcggatt cattttagct atagtttgat 540
tttccctaaa cataaactca tgagaacttc aacagattat attctccaac aacaacgaca 600
atctaattcc acttataggc ctattaatcg cagctacagg aaaatcagca caatttggcc 660
tccacccatg actaccatca gcaatagaag gccctacacc agtttcagca ctactacact 720
caagtacaat agtagttgca ggaattttcc tactgggtccg attccacccc ctccagacta 780
ataataactt tattttaaca actatacttt gcctcggagc cctaaccaca ttattttacag 840
ctatttgtgc tctcacccaa aacgacatca aaaaaatcat tgccttctct acatcaagcc 900
aactaggcct gataatagtg acgctaggaa taaaccaacc acacctagca ttctacaca 960
tctgtaccca cgcattcttc aaagctatac tctttatatg ctctgggtca atcattcata 1020
gcctggcaga cgaacaagac atccgaaaaa taggaaacat cacaaaaatc ataccattca 1080
catcatcatg cctagtaatc ggaagcctcg cctcacagg aataccattc ctaacagggt 1140
tctactcaaa agacctaatt attgaagcaa ttaatacctg caacaccaac gcctgagccc 1200
tactaattac actaatcgcc acttctataa cagctatgta cagcatacga atcattttact 1260
tcgtaacaat aacaaaaaccg cgttttcccc ccctaatttc cattaacgaa aatgacccag 1320
acctcataaa cccaatcaaa cgcctagcat tcggaagcat ctttgcagga tttgtcatct 1380
catataatat tccaccaacc agcattccag tctcacaaat accatgattt ttaaaaaacca 1440
cagccctaatt tatttcagta ttaggattcc taatcgcaat agaactaaac aacctaacca 1500
taaaactatc aataaataaa gcaaatccat attcatcctt ctcaacttta ctgggggttt 1560
tcccattctat tattcacccg attacaccca taaaatctct caacctaaag ctaaaaaacat 1620
ccctaactct cctagacttg atctggttag aaaaaaccat cccaaatcc acctcaactc 1680
ttcacacaaa cataaccact ttaacaacca accaaaaagg cttaattaaa ttgtacttta 1740
tatcattcct aattaacatc atcttaatta ttatcttata ctcaattaat ctcgagtaat 1800
ctcgataata ataaaaatac ccgcaaacaa agatcaccca gctactacca tcattcaagt 1860
agcacaaacta tatattgccc ctaccccaat ccctccttcc aacataactc caacatcatc 1920
aacctcatat atcaaccaat ctcccaaacc atcaagatta attactcaa cttcatcata 1980
ataattaagc acacaaatta aaaaaacctc tataatcacc cccaatacta aaaaacccaa 2040
aattaatcag ttagatcccc aagtctctgg atatttctca gtagctatag cagtcgtata 2100
tccaaacaca accaaccatc cccctaaata aattaaaaaa actattaaac ctaaaaacga 2160
tccaccaaac cctaaaacca ttaaacaacc aacaaaccca ctaacaatta aacctaaacc 2220
tccataaata ggtgaaggct ttaatgctaa cccaagacaa ccaacaaaaa ataatgaact 2280
taaaacaaaa atataattat tcattatttc tacacagcat tcaactgcca ccaatgacat 2340
gaaaaatcat cgttgttaatt caactacaga aacaccattc ggatccatga aaaacacacc 2400
cattatttaa aattattaac cactcattca ttgacctacc tgcccatcc aacatttcat 2460
catgatgaaa ctttgggtcc cttctaggag tctgcctaag agtccaaatc attacagggtc 2520
ttttcttagc catacactac acatcagata caataacagc cttttcatca gtaacacaca 2580
tttgtcgaga cgtaaattac gggtgactaa tccgatatat acacgcaaac ggagcctcaa 2640

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tatttttttat ttgcttatttc cttcatgtcg gacgaggcctt atattatgga tcatatacat2700
ttatagaaac ctgaaacatt ggagtaattc tactgttcgc agtcatagcc acagcattta2760
taggctacgt ccttccatga ggacaaatat cattctgagg tgccacagtt attacaaacc2920
tcctatcagc catcccatat attggaacaa ccctagtcga atgaatttga gggggcttct2880
cagtagacaa agccaccttg acccgattct tcgctttcca cttcatctta ccatttatta2940
tcgcgggccct agcaatcgtt cacctcctct tcctccacga aacaggatca aacaacccaa3000
caggattaaa ctcatagtcga gataaaattc catttcaccc ctactataca atcaaagata3060
tcctagggtat cctaatcata ttcttaattc tcataaccct agtattatct ttcccagaca3120
tactaggaga cccagacaac tacataccag ctaatccact aaacacccca ccccatatta3180
aaccggaatg atatttccta ttgcatagc ccattctacg ctcaatcccc aataaactag3240
gagggtgtcct agccttaatc ttatctatcc taatttttagc cctaataacct ttcttcata3300
cctcaaagca acgaagccta atattccgcc caatcacaca aattttgtac tgaatcctag3360
tagccaacct acctatctta acctgaattg ggggccaaac agtagaacac ccatttatta3420
tcattggcca actagcctcc atctcatact tctcaatcat ctttaattctt ataccaatct3480
caggaattat cgaagacaaa atactaaaat tatatccata aaaaaaaaac acgatcgggt3540
gacatatagg gc 3552

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(2) INFORMATION ON SEQ ID NO. 44:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 601 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

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tttttttttt tttttttttt tgcaattcaa atgaacgttt atttctttaa cccacacaga 60
gtaagggcag agcttagaga tgcctggcac agcatttctc atccaggatc acttcctcgt120
tctttcttct ttgctgggag catcttagat ttatatcatt ttctacaaag acaatatcct180
gaatggcagt cgcagggtta tttcaaagtt ggagtcttct caggaagtag gggagactgg240
attcccagct aatggaattt tcaactgtgat gtctgtgttc tcagtgaatt cttccagaaa300
gccggaggag actgtctcaa catcagtaga gaactcagaa ttctgtttgt ttgcggctgg360
cgtgaagtcc atgatctgct cagagtcagt gcttaaatca tcactctgat aatcctctag420
aggagctttt gtccctctgt atgatccag ttggtcaaag actgagttta gtaggtcaat480
gattgaattc tgtagttctt tattgattga aactaattct gacaggggga aagccacagt540
cagaccacag aagacagtga tcaccaggac cttgaaaagc atcatgtctt agtaggggta600
a 601

```

(2) INFORMATION ON SEQ ID NO. 45:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2147 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

agaaggggaa caaaaaaaaa aatatctgaa ttttgaaaaa ccacaaagct acaacactga 60
ccctctcttt tttttgagac ggagttttgc tcttgttacc caggctggag tgcagtggcg 120
tgatcttggc tcaactgcaac ttccgtctcc cgggttcaag tgattctcct gcctcagcct 180
cccaagtagc tgggtttata ggtgcccgc accagaccgc gctaattttt tagttttagt 240
agagacgggg tttcaccacg ttggccaggc tggctcttaa tgacctctt atttttaact 300
tgataacctg ctattctgcc aaaagacaat ttctagagta gttttgaatg gggtgatttc 360
ccccactccc acaaaactctg aagccagtgt ctagcttact aaaaaaagag ttgtatataa 420
tatttaagat gctgagtgatt tcataggaaa gctgaatgct gctgtaaagt gctctttaag 480
tctttttttt ttttaatccc cttctaataa atgaaactag gggaatttca ggggacagag 540
atgggatttg ttgtatgata aactgtatgt agtttttagt ctttctgttt tgagaagcag 600
tggttggggc atttttaaga tggctggcta ctcttgttt ccctcatgat aataaatttg 660
tcataactca gtaacatgaa cttgccccta gaggtagtgt ttaataattt tgaaatatta 720
aggtcttgcc aagcttctga tgattcacac ctgtactact gattattaag caggacagac 780
tgagctttct gttgcaaata ccttgaggga gaaagtattt tctaaatata cagagaggta 840
acttgacctat atatgttgca tctgtgacct cccttcatat taatatttga taaagatttt 900
aatttatgta aaacttctaa agcagaatca aagctcctct tggggaaatg gcaagtcttt 960
aggataggca agaccctgta tgaatagtag caaagcatta ccgcatggtg gagaacacac 1020
tcgattaaaa atgttaagct atctgaaaaa taaaatgtgc aagtccttcag gatggcaca 1080
aacaaggtt aatgcttctt ggggcacatt tcttagaggg ctgtctgagt gtgtaaatat 1140
aatcgacttt tgtttgtgtt acatgacttc tgtgacttca ttgaaaatct gcacaattca 1200
gtttcagctc tggattactt cagttgacct ttgtgaaggt ttttatctgt gtagaatggg 1260
tgtttgactt gttttagcct attaaatttt tattttcttt cactctgtat taaaagttaa 1320
acttactaaa agaaaagagg tttgtgttca cattaaatgg ttttggtttg gcttctttta 1380
gtcaggcttt ctgaacattg agatatctct aacttagagc tcttcaatcc taagattttc 1440
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tcaggaaaaa cattgccagt tcagtcctttt caaaatgagg gagaaacatt tgccctgcct 1560
gtaataacaa gactcagtag ttatttttta aactgcattt taaaaatttg atagtataat 1620
aacaataagg agtaagccac cttttatagg caccctgtag ttttatagtt cttaatctaa 1680
acattttata tttccttctt ttggaaaaaa cctacatgct acaagccacc atatgcacag 1740
actatacagt gagttgagtt ggctctccca cagtctttga ggtgaattac aaaagtcag 1800
ccattatcat cctcctgagt tatttgaaat gatttttttt gtacattttg gctgcagtat 1860
tggtggtaga atatactata atatggatca tctctacttc tgtattttat tattttatt 1920
tagacctcaa ccacagtctt ctttttcccc ttccacctct ctttgacctg aggatgtact 1980
gtatgtagtc atgcactttg tattaatata ttagaaatct acagatctgt tttgtacttt 2040

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ttataactgtt ggatacttat aatcaaaact ttactaggg tattgaataa atctagctt 2100
actagaaaaa aaaaaaaaaa aaaaaaaaaa ctcaagacta gttctct 2147

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(2) INFORMATION ON SEQ ID NO. 46:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 623 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

cccacgcgtc cccggaaaacg gcggcggcgg cgacaggacc gaggggcctt agttggtggg 60
caagtcgggg atcccagaaa gagaagcgtg acccggaagc ggaaacgggt gtccgtccca120
gtcccgccct gccagtgagc ttctaccatc atggacctat tggtcgggcg ccggaagacg180
ccagaggagc tactgcggca gaaccagagg gccctgaacc gtgccatgcg ggagctggac240
cgcgagcgac agaaactaga gacccaggag aagaaaatca ttgcagacat taagaagatg300
gccaaagcaag gccagatgga tgctgttcgc atcatggcaa aagacttggt gcgcaccccg360
cgctatgtgc gcaagtttgt attgatgcgg gccaacatcc aggtgtgtc cctcaagatc420
cagacactca agtccaacaa ctgatggca caagccatga aggtgtcac caaggccatg480
ggcaccatga acagacagct gaagttgcc cagatccaga agatcatgat ggagtttgag540
cggcaggcag agatcatgga tatgaaggag gagaggattg aattgttgca ttgatgatc600
ccgtgggttt tggggaagtt tta

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623

(2) INFORMATION ON SEQ ID NO. 47:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 781 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

gcgggtatat tgcaagcttg aaaaactaaa agatctgtga aagatgctgc caagaagggc 60
cagaaggatg tctgcatagt tctggccaag gagatgatca ggtcaaggaa ggctgtgagc120
aagctgtatg catccaaagc acacatgaac tcagtgtctca tggggatgaa gaaccagctc180
goggtcttgc gagtggtctg ttccctgcag aagagcacag aagtgtatgaa ggccatgcaa240
agtcttctga agattccaga gattcaggcc accatgaggg agttgtccaa agaaatgatg300
aaggctggga tcatagagga gatgttagag gacacttttg aaagcatgga cgatcaggaa360
gaaatggagg aagaagcaga aatggaaatt gacagaattc tctttgaaat tacagcaggg420
gccttgggca aagcaccagc taaagtgaat gatgcccttc cagagccaga acctccagga480
gcgatggctg cctcagagga tgagggggag gaggaagagg ctctggaggg catgcagtcc540
cggctggcca cactccgcag ctaggggctg cctacccgcg tgggtgtgca cacactcttc600
tcaagagctg ccattttatg tgtctcttgc actacacctc tgttgtgagg actaccattt660
tggagaagggt tctgtttgtc tcttttcatt ctctgccag gttttgggat cgcaaaggga720
ttgttcttat aaaagtggca taaataaatg catcattttt aggaaaaaaa aaaaaaaaaa780
a

```

781

(2) INFORMATION ON SEQ ID NO. 48:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1714 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

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gttgcgacat gcagtgcgcc ggaggaactg tgcctcttga ggccgacgct agggggcccg 60
aagggaact gcgaggcgaa ggtgaccggg gaccgagcat ttcagatctg ctcggtagac 120
ctggtgcacc accaccatgt tggctgcaag gctggtgtgt ctccggacac taccttctag 180
ggttttccac ccagctttca ccaaggcctc ccctgttgtg aagaattcca tcacgaagaa 240

tcaatggctg ttaacaccta gcaggaata tgccacaaaa acaagaattg ggatccggcg 300
tgggagaact ggccaagaac tcaaagaggc agcattggaa ccatcgatgg aaaaaatatt 360
taaaattgat cagatgggaa gatggtttgt tgctggaggg gctgctgttg gtcttggagc 420
attgtgctac tatggcttgg gactgtctaa tgagattgga gctattgaaa aggctgtaat 480
ttggcctcag tatgtcaagg atagaattca ttccacctat atgtacttag cagggaagtat 540
tggtttaaca gcttgtcttg ccatagcaat cagcagaacg cctgttctca tgaacttcat 600
gatgagaggc tcttgggtga caattggtgt gacctttgca gccatgggtg gagctggaat 660
gctggtacga tcaataccat atgaccagag ccagggccca aagcatcttg cttggttgtt 720
acattctggt gtgatgggtg cagtgggtggc tctctgaca atattagggg gtctcttctt 780
catcagagct gcatggtaca cagctggcat tgtgggaggc ctctccactg tggccatgtg 840
tgcgcccagt gaaaagtttc tgaacatggg tgcacccctg ggagtgggct tgggtctcgt 900
ctttgtgtcc tcattgggat ctatgtttct tccacctacc accgtggctg gtgccactct 960
ttactcagtg gcaatgtacg tgggattagt tcttttcagc atgttccctt tgtatgatac 1020
ccagaaagta atcaagcgtg cagaagtatc accaatgtat ggagttcaaa aatatgatcc 1080
cattaaactg atgctgagta tctacatgga tacattaaat atatttatgc gagttgcaac 1140
tatgctggca actggaggca acagaaagaa atgaagtgac tcagcttctg gcttctctgc 1200
tacatcaaat atcttgttta atggggcaga tatgcattaa atagtttgta caagcagctt 1260
tcgttgaagt ttagaagata agaaacatgt catcatattt aaatgttccg gtaatgtgat 1320
gcctcaggtc tgcctttttt tctggagaat aaatgcagta atcctctccc aaataagcac 1380
acacattttc aattctcatg tttgagtgat tttaaaatgt tttggtgaat gtgaaaacta 1440
aagtttgtgt catgagaatg taagtctttt tctacttta aaatttagta ggttcaactg 1500
gtaactaaaa tttagcaaac ctgtgtttgc atattttttt ggagtgcaga atattgtaac 1560
taatgtcata agtgatttgg agctttggtt aagggaccag agagaaggag tcacctgcag 1620
tcttttgttt ttttaaatat ttaggaactt agcacctggg gttatttgga ttaggtgagg 1680
gagcccggta ggaacagccg ggtattgggg aaca

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1714

(2) INFORMATION ON SEQ ID NO. 49:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 831 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

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caccgccagc ccctgctctg aggcaccgag aaacgaggag gcccgtagcg agtctccacg 60
tgggtaccgg cgctctcggc gcccgtagcc acccgccccg cggaagccga catctcgagt120
tctggcagaa gcaatttgcg cggcgaggag cggacgggca ggaacccaat aagctgcttc180
gcctcggagc tgaagcccgt actcaagatg gcggctccgg gcgggcgtgg ccagtgacta240
gaaggcgagg cggcgcgga ccatggcggc ggcgggcgac gagcggagtc cagaggacgg300
agaagacgag gaagaggagg agcagttggt tctggtggaa ttatcaggaa ttattgattc360

agacttcctc tcaaaaatgtg aaaataaatg caagggttttg ggcattgaca ctgagaggcc420
catctcgcaa gtggacagct gtgtctttgc tggggagtat gaagacactc tagggacctg480
tgttatattt gaagaaaatg ttgaacatgc tgatacagaa ggcaataata aaacagtgt540
aaaatataaa tgccatacaa tgaagaagct cagcatgaca agaactctcc tgacagagaa600
gaagggaagg gaagaaaaca taggtggggg ggaatggctg caaataaagg ataatgatt660
ctcctatcga cccaacatga tttgtaactt tctacatgaa aatgaagacg aagaagtgt720
agcttcagcc ccagataaat ctttggaatt ggaagaggaa gagattcaaa tgaaccaccg780
gttcaaacgg gggtttggtg aaccggggga acccattgag ccttggaat t 831

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(2) INFORMATION ON SEQ ID NO. 50:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 744 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

tgaagttctta	agagctttcc	aagtttgga	aggtgtccgg	gttttctgcg	attacttctc	60
tgagcatgaa	cggaagtcac	cctttgtgcc	ttatgcggtg	attttaatga	taggtgtcat	120
ataataggac	gagtaatctg	tttaccattct	gttcttctcg	atgcactcac	aagcgggtaa	180
ctagggtgaca	agaaaacaaa	gatcttattc	aaaagaggtc	ttacagcaac	ccaacgctct	240
atcttcccat	agtaaagatg	acggcgccct	gaggtaaaagt	acaggcaaca	ccactccgcg	300
gtttctcttg	cgccctggtc	caagatggcg	gatgaagcca	cgcgacgtgt	tgtgtctgag	360
atcccggtgc	tgaagactaa	cgccggaccc	cgagatcggt	agttgtgggt	gcagcgactg	420
aaggaggaat	atcagtcctt	tatccggtat	gtggagaaca	acaagaatgc	tgacaacgat	480
tggttccgac	ttgagttcaa	caaggagaag	actcggtggt	ttggaaaatg	ctggttatct	540
catgacctcc	tgaaatatga	gtttgacatc	gagtttgaca	ttcctatcac	atatcttact	600
actgccccag	aaattgagct	tccttgagctg	gatggaaaaga	cagcaaagat	gtacaggtar	
gactgaatag	gagatggcaa	agagtcaaag	aaagccttaa	ggaagaactt	cgtggcgg	
gggagagcat	caggaaagat	agct				

(2) INFORMATION ON SEQ ID NO. 51:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2017 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

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tgagaccoga ggcgcgcgagc aagatggcgg cgcgagtgct gcgcgcccgc ggaggcgctg 60
ggccggggggc ctccctgcagc gggcgggcccc ctgcagcctc ctgcccaggc tccggacatg 120
gacatcttcc agcaacagat ctcgagaaga cagctggcta aaatccttat ttgtccggaa 180
agttgatcca agaaaagatg cccactccaa tctcttagcc aaaaaggaaa caagcaatct 240
atacaaatca cagtttcaca atgttaaacc ggaatgccta gaagcataca acaaaatttg 300
tcaagagggtg ttgccc aaaga ttcacgaaga taaacactac ccttgtaact ttggtggggac 360
ttggaacacg ttggtatggcg agcaggacca agctgtccac ctctggagggt atgaaggagg 420
ctatccagcc ctcacagaag tcatgaataa actcagagaa aataaggaat ttttgggaat 480
tcgtaaggca agaagtgcac tgcttctctc caggaagaat cagctcctgt tggagtccag 540
tttctggaat gagcctgtgc caagatccgg acctaatata tatgaactca ggtcttacca 600
actccgacca ggaaccatga ttgaatgggg caattactgg gctcgtgcaa tccgcttcag 660
acaggatggg aacgaagccg tcggaggatt cttctctcag attgggcagc tgtacatggg 720
gcaccatctt tgggcttaca gggatcttca gaccagggaa gacatacgga atgcagcatg 780
gcacaaacat ggctgggagg aattgggtata ttacacagtt ccacttattc aggaaatgga 840
atccagaatc atgatcccac tgaagacctc gcccctccag taaagctgta ggtttctat 900
gtgcctacat acatttctgt gacaagtatt tgtcgtaaat taattttaat tgtgtatcaa 960
gtgaaaaaga aacactgagg ttttaagctg ctgtatatag cttgtgagaa acctcttttc 1020
tttaaaaattt acataatcac aagaaaggaa agaattacag ttggactgat tgtgacagt 1080
ccttgctgct ctctttgaaa caccocgtgt tgtccagtat accttataac acttagccac 1140
ttctcccccac cctccagaag ggggtccacgt tgaattctga atcatcttga aaataagatt 1200
ccaaccacaa aaaaaattta gccatttctt tactaaaaaa aacaaaaaaa caaatctggt 1260
ttataatcac agatttttag acaaatttct tgtatcagga agaaatacaa attttgtcat 1320
gtttctcaag cagtttttct gagtagtttc tgaggaggaa caaattacaa gtgtacccaal 1380
taactgaaaa tgttttaact cactctcatt tgtaagcagt ccacatagta gacaatgggt 1440
tttccaagct ggccaaggta catttaatca ttaaatcagt ttcacatcat gtattgtgat 1500
gtttcaatgt gagacacaaa aacaatggct tgaaacttgt gtatcatatg tgattttgaa 1560
atgaacacct tgaatagcac taatttttat ttgtggtatt tttctataac aaaacaagta 1620
gctctaggaa aagagggtttt attttgtaaa cgatcatttg tgacctcaga cactctctgg 1680
ctaataatttt aataagctca cagcagataa ttctgagatc atgggtgagg ggtgggtgcat 1740
gttgagattt aaattggcat aaagctgcat accttttgct tagctgtttg atttcatttt 1800
ttaatatagt atgccaattt tgtgactgtt accatgtgaa agtctgtttg aaatgaacaa 1860
ttgtctgccc cacaatcaag aatgtatgtg taaagtgtga ataaatctca tatcaaatgt 1920
caaactttta catgtgaatg attttctcaa agaacataga aaagtcaata aaatcctctt 1980
aatttcacaa aaaaaaaaaa aaaaaaaaaa aaaaaaa

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2017

(2) INFORMATION ON SEQ ID NO. 52:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 856 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

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cgcagtgccg aggcgtgggg ctctctcctt gtcagtcggc gccgcgtgcg ggctgggtggc 60
tctgtggcag cggcgggcggc aggactccgg cactatgagc ggcttcagca ccgaggagcgl20
cgccgcgccc ttctcccttg agtaccgagt ctctctcaaa aatgagaaaag gacaatatat180
atctccattt catgatattc caatttatgc agataaggat gtgtttcaca tggtagttga240
agtaccacgc tggctcaatg caaaaatgga gattgctaca aaggaccctt taaaccctat300
taaacaagat gtgaaaaaag gaaaacttcg ctatgttgcg aatttggtcc cgtataaagg360
atatatctgg aactatgggtg ccatccctca gacttgggaa gaccagggc acaatgataa420
acatactggc tgttggtggg acaatgaccc aattgatgtg tgtgaaattg gaagcaagg480
atgtgcaaga ggtgaaataa ttggcgtgaa agttctaggc atattggcta tgattgacga540
aggggaaacc gactggaaaag tcattgccat taatgtggat gatcctgatg cagccaatta600
taatgatatc aatgatgtca aacggctgaa acctggctac ttagaagcta ctgtggactg660
gtttagaagg tataagggtc ctgatggaaa accagaaaat gagtttgctg ttaatgcaga720
atttaaaagt aaggactttg ccattgatat tattaanaagc actcatgacc attggaaaagc780
attagtgact aagaaaacga atgggaaaag gatcatgttg attgttcaac ttttcggttg840
gccccctcaaa gtgtgc                                     856

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(2) INFORMATION ON SEQ ID NO. 53:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 540 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

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gcatagacaa agggcctcag aatcgcgag ggcgaattgt gccctgggtc gccaaagatgt 60
cgttcccaaa gtataagccg togagcctgc gcactctgcc tgagaccctc gaccagccg120
aatacaacat atctccggaa acccggcggg cgcaagcgag cggttggcca taagagcccal80
gctgaaacga gagtacctgc ttcagtacaa cgatcccaac cgccgagggc tcatcgaaaa240
tcctgccttg cttcggttggg cctatgcaag aacaataaat gtctatccta atttcagacc300
cactcctaaa aactcactca tgggagctct gtgtggattt gggccctca tcttcattta360
ttatattatc aaaactgaga gggataggaa agaaaaactt atccaggaag gaaaattgga420
tcgaacattt cacctctcat attaatctg gcaatgatga ctatatgtat tcctgcctaa480
ataaatcatc tattaatcat taataaaaaa aaaaaaaa aaaaaaaa aaaaaagtcg540
```

(2) INFORMATION ON SEQ ID NO. 54:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1912 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

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tgtgtgagggc ccaacagcgg aatcatcgat gcagggggcct gaattaatgt atctgtgatg 60
ttacagcctt tcgattatga tcccaatgag aaaagtaaac acaggttatg gttcagtccta 120
tgtttgctcc aactgacact tcagatatgg aagcagtatg gaaggaggca aaaccggaag 180
accttatgga ttcaaaaactt agatgtgtgt ttgaattgcc agcagagaat gataaaccac 240
atgatgtaga aataaataaaa attatatcca caactgcac aaagacagaa acaccaatag 300
tgtctaagtc tctgagttct tctttggatg acaccgaagt taagaaggtt atggaagaat 360
gtaagaggct gcaagggtgaa gttcagaggc tacgggaggga gaacaagcag ttcaaggaaag 420
aagatggact gcggatgagg aagacagtgc agagcaacag cccatttca gcattagccc 480
caactgggaa ggaagaaggc cttagcaccg ggctcttggc tctggtggtt ttgttcttta 540
tcgttggtgt aattattggg aagattgcct tgtagaggta gcatgcacag gatggtaaat 600
tggattggtg gatccaccat atcatgggat ttaaaattat cataaccatg tgtaaaaaaga 660
aattaatgta tgatgacatc tcacagggtc tgcctttaa ttacccctcc ctgcacacac 720
atacacagat acacacacac aaatataatg taacgatctt ttagaaagtt aaaaatgtat 780

agtaactgat tgagggggaa aagaatgac tttattaatg acaagggaaa ccatgagtaa 840
tgccacaatg gcataattga aatgtcatct taaacattgg taggccttgg tacatgatgc 900
tgattacct ctcttaaaat gacacccttc ctgcctgtgt ggtgctggcc cttggggagc 960
tgagcccgag catgctgggg agtgcggtca gctccacaca gtagtcccca cgtggcccac 1020
tcccgcccca ggtgctttc cgtgtcttca gttctgtcca agccatcagc tcttgggacl 1080
tgatgaacag agtcagaagc ccaaaggaat tgcactgtgg cagcatcaga cgtactcgtc 1140
ataagtgaga ggctgtgtt gactgattga cccagcgctt tggaaataaa tggcagtgtc 1200
ctgttcactt aaagggacca agctaaattt gtattggttc atgtagtgaa gtcaaaactgt 1260
tattcagaga tgtttaatgc atatttaact tatttaatgt atttcatctc atgtttcttc 1320
attgtcaciaa gagtacagt aatgctgct gctgctgaac tctgttgggt gaactggtat 1380
tgctgctgga gggctgtggg ctctctgttc tctggagagt ctggctatgt ggaggtgggg 1440
tttattggga tgctggagaa gagctgccag gaagtgtttt ttctgggtca gtaataaaca 1500
actgtcatag ggagggaaat tctcagtagt gacagtcaac tctaggttac ctttttaaat 1560
gaagagtagt cagtcttcta gattgttctt ataccacctc tcaaccatta ctcacacttc 1620
cagcggccag gtccaagtct gagcctgacc tccccttggg gacctagcct ggagtcaggal 1680
caaatggatc gggctgcaga ggggttagaag cgagggcacc agcagttgtg ggtggggagc 1740
aaggggaagag agaaactctt cagcgaatcc ttctagtact agttgagagt ttgactgtga 1800
attaatttta tgccataaaa gaccaaccca gttctgtttg actatgtagc atcttgaaaa 1860
gaaaaattat aataaagccc caaaattaaag aaaaaaaaaa aaaaaatact gc 1912

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(2) INFORMATION ON SEQ ID NO. 55:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

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tttttttttt ttttatcgag caagaatctg ttaacagttt tttttttttt tatgttaaat 60
accatgggac aggattgtaa ggatgaaaaa ctcagtcaac aactgcctca caagggataa 120
gaaaaattct gccatgatat tagcaaaggt aaaggaggaa aaatttacac tgtaagaggc 180
accattttcc caaggaatac ctcttgcat ttcctgaatg agtgggatta gcaatctaaa 240
taaatcatat ttcaagaggt aacagcaaca gataaaattt aaagggatta ttaaaataac 300
atttacaaga ctctgaacaa ttcttgaact cttattaaaa ccacaaagaa agaacaattc 360
tttattttatg aatttcataa aggactcaat gtgcaactga catctgctag tgatgatctg 420
gtaatatata acctgtccag tagccgaaca gtttgttttt attgtgtttt ctaaccgtaa 480
gagatcatta aaggcaaagc ctatatgacg ctgtacacac aaaaaaatgg tcaccgtggg 540
ccatactacc aatgaaatgg taggtaaaca aatctttttc tggtaagag aaaaaaaaaa 600
aaaagaaaca gcactctgca tgcttcactc tacaagatga atttccctag aaagaatcca 660

atgaaaaatgg ctgcaattac aacaagaagt gaaggaaagag gactgggtgac attatctctg 720
aaggatggag ttgaggttga tccaggttta tccgaatgtg ctacctttct gagccttaaa 780
ccttcattct tcaggtgcgg attttcttct gatagcttca tcatttctcc ctgaagtcct 840
ttacactctt ccattagttt ccttgtttct gtatcattaa gtgaaacact gtgtggtttt 900
ggcataggto catcttgctt agatgcattc agtggaaacag ctttgctagg ttccatatca 960
ttcaatttat catcttcatt gggcatttca aatacgcac tcaatttgga atccattaat 1020
tcatacaggt ttgctctctt ccacacagct tccatatctg aagtgtttgg tggagcaaaa 1080
attgtctgta ccataaactt gtgtttactc ttttcattcg gatcatagtc aaagggtctg 1140
agcattactg aaacagtcac agttgacctt gggtaataa ttccactgtt gggcctcacal 1200
cagtaccggc gaggtgctgt agtcttcaat ttgaaacaca cttttctatc cgatggattt 1260
cgcaattttaa gatttgtagt gactacatct gtgaaggggc ctttgaattt gaggtctgtg 1320
ggcggatcga ggaccaggat ctgctcgtct tcgccatggc ccctgaggcg gacgccatcg 1380
gagagacagc gcagagcagg gggcggtctg ctgctgggg gcgggggacg atggcgagag 1440
gggaggggga gcgagttcgc atctctctct ttcctgggta gactctgttc aaccacattc 1500
ttatgttggc agatctgctt ccagattgat ttttagagca ccatacttt cacttctctg 1560
attctgattt tgttttgtt tgtttgggtt ttctgaaact taaaatgctg ccccgaaaaa 1620
actatatttt tgagtttgtg ttctgaaagc ctccgtgctg ctggatcttt ggggggaaat 1680
acaggatcct tcagcactga ggtgtttaag atttgcaact agcaatgcaa ttttttctaa 1740
atatggggat atttacctt attaagaaat tatactaaac attgatgtcc ttgatcattt 1800
tatgttctca tattactttt gattctacta tgattgtgtg gtggtgaaca aagatcattt 1860
caaaacaaaaa ctgtaatttt gttatatttg attcaatgga atttacctaa aaaataaaga 1920
ctaaaaatgt gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa
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(2) INFORMATION ON SEQ ID NO. 56:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

cggetcgagc ggctcgagat tcgaggtcgt ggtggtcttg gaagagcgtc gagggggccg 60
tggacgtgga atgggcccag gagatggatt tgattctcgt ggcaaacgtg aatttgatag 120
gcatagtgga agtgatagat ctggcctgaa gcacgaggac aaacgtggag gtagcggatc 180
tcacaactgg ggaactgtca aagacgaatt aacagagtcc cccaaatata ttcagaaaca 240
aatatcttat aattacagtg acttgatca atcaaagtgt actgaggaaa cacctgaagg 300
tgaagaacat catccagtgg cagacactga aaataaggag aatgaagttg aagaggtaaa 360
agaggagggt ccaaaagaga tgactttgga tgagtgggaag gctattcaaa ataaggaccg 420
ggcaaaagta gaatttaata tccgaaaacc aaatgaaggt gctgatgggc agtggaaaga 480

gggatttggt cttcataaat caaagagtga agaggctcat gctgaagatt cggtttatgga 540
ccatcatttc cggaagccag caaatgatat aacgtctcag ctggagatca attttgaga 600
ccttgggccgc ccaggacgtg ggggcagggg aggacgaggt ggacgtgggc gtggtgggcg 660
cccaaacctt ggcagcagga ccgacaagtc aagtgtctct gctcctgatg tggatgacct 720
agaggcattc ccagctctgg cttaactgga tgccataaga caaccctggt tcccttgtga 780
acccttctgt tcaaagcttt tgcattgctta aggattccaa acgactaaga aattaaaaaa 840
aaaaagactg tcattcatat cattcacacc taaagactga attttatctg ttttaaaaat 900
gaacttctcc cgctacacag aaqtaacaaa tatggtagtc agttttgtat ttagaaatgt 960
attggttagc gggatgtttt cataattttc agagattatg cattcttcat gaatactttt 1020
gtattgctgc ttgcaaatat gcatttccaa acttgaaata taggtgtgaa cagtgtgtac 1080
cagtttaaaag ctttcacttc atttgtgttt ttaattaag gatttagaag tcccccaat 1140
tacaaactgg ttttaaatat tggacatact ggttttaata cctgctttgc atattcacac 1200
atggtcaact gggacatggt aaactttgat ttgtcaaatt ttatgctgtg tggaaatact 1260
actatatgta ttttaactta gttttaatat ttccattttt ggggaaaaat tttttttcac 1320
ttctcatgat agctgttata tatatatgct aaatctttat atacagaaat atcagtactt 1380
gaacaaattc aaaagcacat ttggtttatt aaccctgtgc tgccctggca tggggcccat 1440
ttgggggtcca aattataa
1458

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(2) INFORMATION ON SEQ ID NO. 57:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2188 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

gggccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 60
ccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 120
ccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 180
ccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 240
ccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 300
ccaaaccctcc cccacccccc cccctacaag tcacctgggt aagccaacct gaattctact 360
cacctgggagc tggaggtatg tatgacagaa tgcgacgagg aggtgatgga tatgatgggt 420
gttatggagg ttttgatgac tatggtggct ataataatta cggctatggg aatgatggct 480
ttgatgacag aatgagagat ggaagaggta tgggaggaca tggctatggg ggagctgggt 540
atgcaagttc aggttttcat ggtggtcatt tcgtacatat gagagggttg ctttttcgtg 600
caactgaaaa tgacattgct aatttcttct caccactaaa tccaatacga gttcatattg 660
atattggagc tgatggcaga gccacaggag aagcagatgt agagtttgtg acacatgaag 720
atgcagtagc tgccatgtct aaagataaaa ataacatgca acatcgatat attgaactct 780
tcttgaattc tactcctgga ggcggtctct gcatgggagg ttctggaatg ggaggctacg 840

gaagagatgg aatggataat cagggaggct atggatcagt tggagaatg ggaatgggga 900
acaattacag tggaggatat ggtactcctg atggtttggg tggttatggc cgtgggtggg 960
gaggcagttg aggttactat gggcaaggcg gcatgagtgg aggtggatgg cgtgggatgt 1020
actgaaagca aaaacacca cacaacagtc ttgacaacag catctggtct actagacttt 1080
cttacagatt taatttcttt tgtattttta gaactttata atgactgaag gaatgtgttt 1140
tcaaaatatt atttggtaaa gcaacagatt gtgatgggaa aatgttttct gtaggtttat 1200
ttgttgcata ctttgactta aaaataaatt tttatattca aaccactgat gttgatactt 1260
tttatatact agttactcct aaagatgtgc tgccttcata agatttgggt tgatgtattt 1320
tactattagt tctacaagaa gtatgtgggt gtaattttag aggataatgg ttcacctctg 1380
cgtaaactgc aagtcttaag cagacatctg gaatagagct tgacaaaataa ttagtgtaac 1440
ttttttcttt agttcctcct ggacaacact gtaaatataa agcctaaaga tgaagtggct 1500
tcaggagtat aaattcagct aattatttct atattattat ttttcaaagt tcatttatca 1560
ggcatagctc tgaaacattg atgatctaag aggtattgat ttctgaatat tcataattgt 1620
gttacctggg tatgagagtg ttggaagctg aattctagcc ctgatttttg gagtataaac 1680
ccttcagcac ttgaccgaaa taccaaaaat gtctccaaaa aattgatagt tgcaggttat 1740
cgcaagatgt cttagagtag ggttaagggt ctgagtgaac caagaattca gtattaaagt 1800
cataggtatt tactatggag tataattctc acaattgtat tttcagtttt ctgcccataa 1860
gagtttaaat aactgtataa atgatgactt taataaaatg taagcaacaa gtccatgtca 1920
tagtcaataa aaacaatcct gcagttgggt tttgtatctg atccctgctt ggagttttag 1980
tttaaaagaa ctatatgtag caaggaaaag gtgcttttta attttaatcc ctttgatcaa 2040
tatggctttt ttccaaattg gctaattgat caaaatgaaa cctgttgatg tgaattcagt 2100
tattgaactt gttacttgtt tttgccagaa atgttattaa taaatgtcaa tgtgggagat 2160
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa

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2183

(2) INFORMATION ON SEQ ID NO. 58:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1548 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

ctcgctagtt cgatcggtag cgggagcgga gagcggaccc cagagagccc tgagcagccc 60
caccgccgcc gccggcctag ttaccatcac accccgggag gggccgcagc tgccgcagcc 120
ggccccagtc accatcacccg caaccatgag cagcgaggcc gagaccagc agccgcccgc 180
ggcccccccc ggggcccccg ccctcagcgc cgccgacacc aagcccgga ctacgggcag 240
cggcgcaggg agcgggtggc cgggcgccct cacatcggcg gcgcctgccg gcggggacaa 300
gaaggtcatc gcaacgaagg ttttggaac agtaaaatgg ttcaatgtaa ggaacggata 360
tggtttcatc aacaggaatg acaccaagga agatgtatgt gtacaccaga ctgccataaa 420

gaagaataaac ccaggaagt accttcgcag tgtaggagat ggagagactg tggagtttga 480
tgttgtgaa ggagaaaagg gtgcggaggc agcaaatgtt acaggtcctg gtggtgttcc 540
agttcaaggc agtaaatatg cagcagaccc taaccattat agacgctatc cacgtcgtag 600
gggtccctcc cgcattacc agcaaaatta ccagaatagt gagagtgggg aaaagaacga 660
gggatcggag agtgctcccg aagccaggc ccaacaacgc cggccctacc gcaggcgaag 720
gttccacact taactacatg ggagacccta tgggcgtcga ccacagtatt ccaaccctcc 780
tgtgcaggga gaagtgatgg aggtgtctga caaccagggt gcaggagaac aaggttagacc 840
agtgaggcag aatatgtatc ggggatatag accacgattc cgcaggggcc ctccctcgcca 900
aagacagcct agagaggacg gcaatgaaga agataaagaa aatcaaggag atgagacca 960
aggtcagcag ccacctcaac gtcggtaccg ccgcaacttc aattaccgac gcagacgccc 1020
agaaaaccct aaaccacaag atggcaaaga gacaaaagca gccgatccac cagctgagaal 1080
ttcgtccgct ccgaggctg agcagggcgg ggctgagtaa atgccggctt accatctctal 1140
ccatcatccg gtttagtcat ccaacaagaa gaaatatgaa attccagcaa taagaaatga 1200
acaaaagatt ggagctgaag acctaaagt cttgtttttt gcccgttgac cagataaatal 1260
gaactatctg cattatctat gcagcatggg gtttttatta tttttacctt aagacgtctc 1320
tttttggtaa taacaaacgt gtttttttaa aaagcctggg tttttctaat acgcttttaa 1380
aggtttttaa attgtttcat atctggtcaa gttgagatgt ttaagaactt catttttaat 1440
ttgtaataaa agtttacaac ttgatttttt caaaaaagtc aacaaactgc aagcacctgt 1500
taataaaggc cttaataaat tgtctttgtg taaaaaaaaa gggaatat 1548

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(2) INFORMATION ON SEQ ID NO. 59:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1254 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

ggaccgcttc ccccgagcca gcagcagcgt ttgacgtcat cgtgcgtgtg gtgccctgc 60
tgccgggggt ggtgattgga ggaaaccccg tgtctgacgg agggctgtag cctgtgagca 120
gcgagatcca gggacagagt ctcagcctcg ccgctgctgc cgccgccgcc gccagagac 180
tgctgagccc gtccgtccgc cgccaccacc cactccggac acagaacatc cagtcattga 240
taaaaatgag ctggttcaga aggccaaact ggccgagcag gctgagcgat atgatgacat 300
ggcagcctgc atgaagtctg taactgagca aggagctgaa ttatccaatg aggagaggaa 360
tcttctctca gttgcttata aaaatgttgt aggagcccgt aggtcatctt ggaggggtcgt 420
ctcaagtatt gaacaaaaga cggaagggtgc tgagaaaaaa cagcagatgg ctcgagaata 480
cagagagaaa attgagacgg agctaagaga tatctgcaat gatgtactgt ctcttttgga 540
aaagtctctg atccccaatg cttcacaagc agagagccaa agtcttctat ttgaaaatga 600
aaggagatta ctaccgttac ttggctgagg ttgccgctgg tgatgacaag aaagggattg 660
tcgatcagtc acaacaagca taccaagaag cttttgaaat cagcaaaaaa gaaatgcaac 720

caacacatcc tatcagactg gggctggccc ttaacttctc tgggttctat tatgagattc 780
tgaaactccc cagagaaaagc ctgctctctt gcaaagacag cttttgatga agccattgct 840
gaacttgata cattaagtga agagtcatac aaagacagca cgctaataat gcaattactg 900
agagacaact tgacattgtg gacatcggat acccaaggag acgaagctga agcaggagaa 960
ggaggggaaa attaaccggc cttccaactt ttgtctgcct cattctaaaa ttacacaggt 1020
agaccatttg tcatccatgc tgtcccacaa atagtttttt gtttacgatt tatgacaggt 1080
ttatgttaac tctatttgaa tttctatatt ttccctgtgg gttttatgtt tagttttggg 1140
ggagtaggag ccagttaaac gtttggggag tttgtctgtt tttcgtcttt gaggggtggg 1200
ccagtatggg ggggtgttgg gatattttgt taccagtttt tgaggtgttt ttgg 1254

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(2) INFORMATION ON SEQ ID NO. 63:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 954 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

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cctcttcttt ttctttttct tctttttttt ttctttttt ttttttgtga gagcaggggc 60
actttattgg tatagagact gcagaggggac caggggcttt agctgttggc agctatgggtg120
tccttaatcc agtccacata gttgtagacc ttgggtgtaga ctccaggcct gttcttctgg180
gcacagccat agccccagga gacaattcct tggagctctc cattggagac cacagggcca240
ccagaatcac cctggcagga atccttgccct ccctcgagga agcccacaca gaacatgttg300
ttggtaatct ttccagggtg ggaggcttca cactcagcct ggctcagcac aggagcatcc360
aggcactgca gctcgtctgg gtagtcggca ccagaactca gagtgttggc ccagccggag420
atgagggact cgggtgccagc agctggaggg gcagtgaggc gagagatggc ggacacgcgg480
gaattgatga cggcaggtga ggagagcttg atcagcagga tgtcattgtc cagagtcagg540
ctgttgtatt tgggggtggcg gatgatcttg gccgcattga tgaactgttc attcccctcc600
aggacttcga tgttgtgtc tcccagctc acctggatgc gggacttgta gcagtgcact660
gctgacacca cccactgttc gctgatgagg gagccaccgc agaagtggta gccagaattc720
aaggacacct ggtagggggac agaattctcc tcacagatgt agcccccaac gatcttgtca780
tcatcatcaa aggggggcagc aacagcagct gcaacaaagg taaggatcag aagtagattc840
atggtggtag agtgtgcctg attgctgggt gagaaccctt ctttatacct cccgaggatg900
gggagaggag gtgtctgtga ggtgagggtc actgctcctc ccagcacaaa caca 954

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(2) INFORMATION ON SEQ ID NO. 65:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2213 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

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ggcgggacccg ccggggggtcg aggcctgcct ctccgagagc tccctggcgcg gccgtccccg 60
cccggggccc caggtgcgct tcccctagag agggattttc cgggtctcgtg ggcagaggaa 120
caaccaggaa cttgggggtc agtctccacc ccacagtggg gcggatccgt cccggataag 180
accgcgtgtc tggccctgag tagggtgtga cctccgcagc cgcagaggag gacgcagcc 240
ggcctcgaag aacttctgct tgggtggctg aactctgac ttgacctaga gtcattggcca 300
tggcaaccaa aggaggtact gtcaaagctg ctccaggatt caatgccatg gaagatgccc 360
agaccctgag gaaggccatg aaagggtctg gcaccgatga agacgccatt attagcgtcc 420
ttgcctaccg caacaccgcc cagcgccagg agatcaggac agcctacaag agcaccatcg 480
gcagggactt gatagacgac ctgaagtcag aactgagtgg caacttcgag caggtgattg 540
tggggatgat gacgcccacg gtgctgtatg acgtgcaaga gctgcgaagg gccatgaagg 600
gagccggcac tgatgagggc tgcctaattg agatcctggc ctcccggacc cctgaggaga 660
tccggcgcat aagccaaacc taccagcagc aatatggacg gagccttgaa gatgacattc 720
gctctgacac atcgttcatg ttccagcgag tgctgggtgtc tctgtcagct ggtgggaggg 780
atgaaggaaa ttatctggac gatgctctcg tgagacagga tgcccaggag ctgtatgagg 840
ctggagagaa gaaatggggg acagatgagg tgaaatttct aactgttctc tgttcccga 900
accgaaatca cctgttgcat gtgtttgatg aatacaaaag gatatacag aaggatattg 960
aacagagtat taaatctgaa acatctggta gctttgaaga tgctctgctg gctatagtaa1020
agtgcattag gaacaaatct gcataatttg ctgaaaagct ctataaatcg atgaagggt1080
tgggcaccga tgataacacc ctcatcagag tgatggtttc tcgagcagaa attgacatgt1140
tggatatccg ggcacacttc aagagactct atggaaagtc tctgtactcg ttcatcaagg1200
gtgacacatc tggagactac aggaaagtac tgcttgttct ctgtggagga gatgattaaa1260
ataaaaaatc cagaaggaca ggaggattct caacactttg aattttttta acttcatttt1320
tctacactgc tattatcatt ctgtattatt attcacctat aattagtcatt tatgatgctt1440
cctcctagaa tatagactgt ctgtattatt agatataaat ggagatttta aagtagaaat1500
taaagctgta cttgcatttc aaagcttata ctttctactt tgtgtttcac agacattgaa1560
aatattgtaa tttccatat tttcttttca gtgaaaaatt ttttaaatgg aagactgttc1620
taaaatcact tttttcccta atccaatttt tagagtggct agtagtttct tcatttgaaa1680
ttgtaagcat ccggtcagta agaatgccca tccagttttc tatatttcat agtcaaagcc1740
ttgaaagcat ctacaaatct ctttttttag gttttgtcca tagcatcagt tgatccttac1800
taagtttttc atgggagact tcttcatca catcttatgt tgaaatcact ttctgtagtc1860
aaagtatacc aaaaccaatt tatctgaact aaattctaaa gtatggttat acaaaccata1920
tacatctggt taccaaacat aaatgctgaa cattccatat tattatagtt aatgtcttaa1980
tccagcttgc aagtgaatgg aaaaaaaaaa aagcttcaaa ctagggtattc tgggaatgat2040
gtaatgctct gaatttagta tgatataaag aaaacttttt tgtgctaaaa atacttttta2100
aaatcaattt tgttgattgt agtaatttct atttgcactg tgcttttcaa ctccagaaac2160
attctgaaga tgtacttgga ttttaattaaa aagttcactt tgtaaaaaaa aaa 2213

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(2) INFORMATION ON SEQ ID NO. 67:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2878 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

cctcgtgcag gtgcacogct tggtcctaaa agctctggag gatggccggg .catatgggtc 60
tccatgggtgc aacaaacaga tcacaagggtg cctaattgaa tgcgagatg aatataaata 120
taatgtggag gctgtggagc tgctaattcg caatcatttg gttaatatgc agcagtatga 180
tcttcaccta gcgcagtgcaa tggagaatgg cttaaactac atggctgtgg catttgctat 240
gcagttagta aaaatcctgc tgggtgatga aaggagtgtt gctcatgtta ctgaggcaga 300
tctgttccac accattgaaa cctcatgag gattaatgct cattccagag gcaatgctcc 360
agaaggattg ccccagctga tggaaagtagt gcgatccaac tatgaagcaa tgattgatcg 420
tgctcatgga ggcccaaaact ttatgatgca ttctgggac tctcaagcct cagagtatga 480
tgaccctcca ggccgtgagg agaaggcaga gtatcttctg agggaaatggg tgaatctcta 540
ccattcagca gcagctggcc gcgacagtac caaagcttct tctgcatttg ttggacagat 600
gcaccagcaa ggaatactga agaccgatga tctcataaca aggttcttct gtctgtgtac 660
tgaaatgtgt gttgaaatca gttaccgtgc tcaggctgag cagcagcaca atcctgctgc 720
caatcccacc atgatccgag ccaagtgtta tcacaacctg gatgccttgg ttcgactcat 780
tgactgtctc gtgaaacact caggggaggc caccaacact gtcacaaaga ttaatctgct 840
gaacaaggtc cttggtatag tagtgggagt tctccttcag gatcatgatg ttcgtcagag 900
tgaatttcag caacttccct accatcgaat ttttatcatg cttctcttgg aactcaatgc 960
acctgagcat gtgttggaac ccattaattt ccagacactt acagcttctt gcaatacatt1020
ccacatcttg aggcctacca aagctcctgg ctttgtatat gcctggcctg aactgatttc1080
ccatcgata tttattgcaa gaatgctggc acatacgcca cagcagaagg ggtggcctat1140
gtatgcacag ctactgattg atttattcaa atatttagcg ccttctctta gaaatgtgga1200
actcaccaaa cctatgcaaa tcctctacaa gggcacttta agagtgtctg tggttctttt1260
gcagtatttc ccagagttcc tttgtgatta ccattatggg tctgtgatg tgatcccacc1320
taattgtatc cagttaaagaa atttgatcct gatgccttt ccaagaaaca tgaggctccc1380
cgaccctatc actcctaata taaagggtgga catgttgagt gaaattaaca ttgctccccg1440
gattctcacc aatttctact gagtaatgcc acctcagttc aaaaaggatt tggattccta1500
tcttaaaact cgatcaccag tcactttcct gtctgatctg cgcagaacct acaggtatcc1560
aatgaacctg ggaatcgcta caacctccag ctcatcaatg cactgggtgt ctatgtcggg1620
actcaggcca ttgcgcacat ccacaacaag ggcagcacac cttcaatgag caccatcact1680
cactcagcac acatggatat cttccagaat ttggctgtgg acttgacac tgagggtcgc1740
tatctctttt tgaatgcaat tgcaaatcag ctccgggtacc caaatagcca cactcactac1800

ttcagttgca ccatgctgta cctttttgca gaggccaata cggaagccat ccaagaacag1860
atcacaagag ttctcttggg acggttgatt gtaaataaggc cacatccttg ggtctctctt1920
attaccttca ttgagctgat taaaaaccca gcgtttaagt tctggaacca tgaatttgta1980
cactgtgccc cagaaatcga aaagtatttc cagtcggtcg cacagtgtg catgggacag2040
aagcaggccc agcaagtaat ggaagggaca ggtgccagtt agacgaaact gcactctgt2100
tgtacgtgtc agtctagagg tctcactgca ccgagttcat aaactgactg aagaatcctt2160
tcagctcttc ctgaactttcc cagcccttgg gtttgtgggt atctgcccca actactgttg2220
ggatcagccc cctgtcttat gtgggcacgt tccaaagttt aaatgcattt tttgactct2280
tggccaaaat ttagaagatg ctgtgaatat cattttgaac ttgtgtaaat acatgaaaga2340
ggaaaaacct tgtctggaac ttcttggtt tgtgcaagct gtgtccaagg caagtacata2400
aactggtagc ttgtaatgaa gaggcagctg atgccatgca cttgtctgag ggcatagtct2460
catgtctctt gacattcctg gtgtcccaaa gaatagcaaa aagccagttt gaattatgt2520
taacttattt ttttaatgtg gacaggggac cttgaaaatc actaagttat taaaaatgt2580
gatgtgctag aattggatat gtccaggaac atgggaaggg ctactattg gaatccatgt2640
agtcttccat ttgtctctac ccaaacgtat tccaaagctg actgcatttg taccatctta2700
tttcttttgg ggattataca cctcagccgc ctgagatggg ggtcagctct ttatataaag2760
ggaaaccaga ccaggcctaa agcccacccc ctaccctcac cccccccaca atcctctct2820
gaaactttta aaaccagtgg ggatttttagg gaaagggaac ccaaaccgca attaatgt 2878

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(2) INFORMATION ON SEQ ID NO. 68:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 701 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```

atgatatttt ggatgtagtc ttttgattgt ttaaattctta aaaagtaatg ggatcttttg 60
acactggggt atgttttatt tttatgtgtg caaattttta ccatattctt ttctagttaa120
agaggaaaaa gcaagttgct ccagaaaaac ctgtaaaagaa acaaaaagaca ggtgagactt180
cgagagccct gtcattcttc aaacagagca gcagcagcag agatgataac atgtttcaga240
ttgggaaaat gaggtacgtt agtgttcgcg attttaaaagg caaagtgcga attgatatta300
gagaatattg gatggatcct gaaggtgaaa tgaaaccagg aagaaaagggt atttctttta360
atccagaaca atggagccag ctgaaggaac agatttctga cattgatgat gcagtaagaa420
aactgtaaaa ttcgagccat ataaataaaa cctgtactgt tctagttggt ttaatctgtc480
tttttacatt ggcttttggt ttctaaatgt tctccaagct attgtatggt tggattgcag540
aagaatttgt aagatgaata ctttttttta atgtgcatta ttaaaaaatat tgagtgaagc600
taattgtcaa ctttattaag gattactttg tctgccacc acctagtgtg aaataaaatc660
aagtaataca atcttaaaaa aaaaaaaaaa aaaagtcgag c 701

```

(2) INFORMATION ON SEQ ID NO. 69:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 817 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```

gttttttttt tttttttttt ttttttttaa gcacagaaaag cttttattac cacagaggaa 60
atcaggaaat gctggaggca gcctcgtag ctgtgtgatc agggagggga cagcaggcgg120
gaaccctgtca tcaatcatgt ctgggcagtc tcccaaccaa caggtttggt tggttcaggal80
gaggcttttg ctgggctgtg tgtgtgtatg atcaggaagg tcagcctcaa caaatgggct240
tcttcctgga cataggacag ccagaatcgg ggacaccagc tgcacagaca ccaccttaaa300
atggaaatca aattagggttc attacatcag gaagtacatt tcaccctgat cataaaagag360
ggacaaggga gcactgggct ctactggata gcctttcttt tagataagat gcttttaaaa420
gttaaacatt ggcagggcct ttcccctagc taacagcaag cagcacacaa ttccaagtca480
gcttgtaaaag cttttgttat ctttgttatc tgttattatt tggattttga acgaaattga540
tggagtacga gccggttagag gaatcctggt tgatctggaa attttccgtg gagagcccaa600
aaggctcggag aaccaagttc ccaagatctt ttaatttacc taacatctct tcttttagtc660
tttcattacg ttcttcaatt tgcttaggta atctcataca agcttctctt gcttgatgta720
ttgatgaagg ttcccgcctg ctgtcccctc cctgatcaca cagctaacga ggctcctcca780
gcatttcctg atttcctctg tggtaataaa agctttc 817

```

(2) INFORMATION ON SEQ ID NO. 70:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2686 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

```

gcaaggccta ctgtcggctg ggaggggagg tgtagccggt ctttgggggt aggcggtagt 60
ggcggaagag gttcggcggc tgatggcgga tcaggatcgg aagcctgcgt aactttctcc 120
cttgatccgg gagtctttcc actggattca caatgacatc ctttcaagaa gtccatttgc 180
agacttccaa ctttgcccat gtcatctttc aaaatgtggc caagagttac cttcctaattg 240
cacacctgga atgtcattac accttaactc catatatcca tccacatcca aaagattggg 300
ttggtatatt caaggttggg tggagtactg ctctgtatta ttacacgttt ttatgggtccc 360
ctatgcctga acattatgtg gaaggatcaa cagtcaattg tgtactagca ttccaaggat 420
attaccttcc aaatgatgat ggagaatttt atcagttctg ttacgttacc cataagggtg 480
aaattcgtgg agcaagtaca cctttccagt ttcgagcttc ttctccagtt gaagagctgc 540
ttactatgga agatgaagga aattctgaca tgttagtggg gaccacaaaa gcaggccttc 600
ttgagttgaa aattgagaaa accatgaaaag aaaaagaaga actgttaaaag ttaattgccg 660
ttctggaaaa agaaaacagca caacttcgag aacaagttgg gagaatggaa agagaactta 720
acctatgaaa agaaaagatgt gaccaactgc aagcagaaca aaagggtctt actgaagtaa 780
cacaaagctt aaaaatggaa aatgaagagt ttaagaagag gttcagtgat gctacatcca 840
aagcccatca gcttgaggaa gatattgtgt cagtaacaca taaagcaatt gaaaaagaaa 900
ccgaattaga cagtttaaaag gacaaaactc agaaggcaca acatgaaaga gaacaacttg 960
aatgtcagtt gaagacagag aaggatgaaa aggaacttta taaggtaacat ttgaagaata 1020
cagaaaataga aaataccaag cttatgtcag aggtccagac tttaaaaaat ttagatggga 1080
acaaagaaaag cgtgattact catttcaaag aagagattgg caggctgcag ttatggttgg 1140
ctgaaaagga aaatctgcaa agaactttcc tgcttacaac ctcaagtaaa gaagatactt 1200
gtttttttaa ggagcaactt cgtaaaagcag aggaacaggt tcaggcaact cggcaagaag 1260
ttgtctttct ggctaaagaa ctcaagtgat ctgtcaacgt acgagacaga acgatggcag 1320
acctgcatac tgcacgcttg gaaaacgaga aagtgaaaaa gcagttagct gatgcagtg 1380
cagaaacttaa actaaatgct atgaaaaaag atcaggacaa gactgataca ctggaacacg 1440
aactaagaag agaagttgaa gatctgaaac tccgtcttca gatggctgca gaccattata 1500
aagaaaaatt taaggaatgc caaaggctcc aaaaacaaat aaacaaactt tcagatcaat 1560
cagctaataa taataatgtc ttcacaaaga aaacggggaa tcagcagaaa gtgaatgat 1620
cttcagttaa cacagacca gccacttctg cctctactgt agatgtaaa gccatcacct 1680
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aaattgtctg aaaaacagaa aagtataata aatgtaaaca actcttgca gtagaagaag 1800
caaaatgcaa taaatatgct gatgaacttg caaaaatgga gctgaaatgg aaagaacaag 1860
tgaaaaattg tgaaaaatgt aaacttgaac tagctgaagt acaggacaat tataagaac 1920
ttaaaaggag tctagaaaat ccagcagaaa ggaaaatgga agatggagca gatggtgct 1980
tttaccaga tgaaatacaa aggccacctg tcagagtcct ctcttgggga ctggaagaca 2040
atgttgctg cagccagcct gctcgaaact ttagtgcgcc tgatggctta gaggactctg 2100
aggatagcaa agaagatgag aatgtgccta ctgctcctga tcctccaagt caacatttac 2160
gtgggcatgg gacaggcttt tgctttgatt ccagctttga tgttcacaag aagtgtcccc 2220
tctgtgagtt aatgtttcct cctaactatg atcagagcaa atttgaagaa catgttgaaa 2280
gtcactggaa ggtgtgccc atgtgcagcg agcagttccc tcctgactat gaccagcagg 2340
tgtttgaaa gcatgtgcag acctattttg atcagaatgt tctaaatttt gactagttac 2400
tttttattat gagttaatat agtttagcag taaaaaaaaa aaaaaaaacc acacctaaaa 2460
tagaccactg aggagaccat agagcggatg ctttcatgca ccctttactg cactttctga 2520
ccaggagcta ctttgagttt ggtgttacta ggatcagggt cagtctttgg cttatcaata 2580
aattttaatc tctgttaatc ttaccaaata ttaaaaaaaa aaaaaaaat cgtactttat 2640
ttatccctag ttgcagactg ctgaataaag gtcaaggatt atccat 2686

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(2) INFORMATION ON SEQ ID NO. 72:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 922 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```

ctgctctgaa aagccatctt tgcattgttc ctcacccgcc tccttgctcg cggcagccgc 60
ctccgcgcgc cgcctcctcc gccgcgcgcg actccggcag ctttatcgcc agagtccctg120
aactctcgct ttctttttta tcccttgcac cggatcaccg gcgtgcccc aatgtcaga180
cgcagccgta gacaccagct ccgaaatcac caccaaggac ttaaaggaga agaaggaagt240
tgtggaagag gcagaaaatg gaagagacgc ccctgctaac gggaatgcta atgaggaaaa300
tggggagcag gaggctgaca atgaggtaga cgaagaagag gaagaagggg ggtgatggtg360
aggaagagga tggagatgaa gatgaggaag ctgagtcagc tacgggcaag cgggcagctg420
aagatgatga ggatgacgat gtcgatacca agaagcagaa gaccgacgag gatgactaga480
cagcaaaaaa ggaaaagtta aactaaaaaa aaaaaggccg ccgtgacctt ttcacctcc540
acttcccgtc tcagaatcta aacgtggtca ccttcgagta gagaggcccg cccgcccacc600
gtgggcagtg ccacccgcag atgacacgcg ctctccacca cccaacccaa accatgagaa660
tttgcaacag gggagggaag aaggaccaaa acttccaagg ccctgctttt tttcttaaaa720
gtacttttaa aaggaaattt gtttgatgtg tctatttaca tttgatagtg ttgtacatat780
tgttaggggt caaccatttt taatgatctc ggatgaccaa accagccttc ggaagcgttc840
tctggcctac ttctggactt ttacgttggg gggttgttga ccatgttcaa ttataatccc900
aaaaggggga aaaaaaacct tt

```

922

(2) INFORMATION ON SEQ ID NO. 73:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 870 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

ggaagtggcg gtgcgagggc tgctgcacag cgagcggagc cgcgggtccg acggcagcgc 60
gtgccccgag ctctccgcct cccccgcgcc gccagccgag gcagctcgag cccagtcgcgc120
ggccccagca gcagcgccga gagcagcccc agtagcagcg ccatggccgg gtggaacgcc180
tacatcgaca acctcatggc ggacggggacc tgtcaggacg cggccatcgt ggggtacaag240
gactcgccct ccgtctgggc cgcggtcccc gggaaaaacgt tcgtcaacat cacgccagct300
gaggtgggtg tcctggttgg caaagaccgg tcaagttttt acgtgaatgg gctgacactt360
ggggggccaga aatgttcggt gatccgggac tcaactgctgc aggatgggga atttagcatg420
gatcttcgta ccaagagcac cggtaggggcc cccaccttca atgtcactgt caccaagact480
gacaagacgc tagtcttgcg gatgggcaaa gaaggtgtcc acggtgggtt gatcaacaag540
aaatgttatg aaatggcctc ccaccttcgg cgttcccagt actgacctcg tctgtccctt600
ccccctcacc gctccccaca gctttgcacc cctttcctcc ccatacacac acaaaccatt660
ttattttttg ggccattacc ccataccctt tattgctgcc aaaaccacat gggctggggg720
ccagggctgg atggacagac acctccccct acccatatcc ctcccgtgtg tggttggaaa780
acttttgttt tttggggttt tttttttctg aataaaaaag attctactta aaaaaaaaaa840
aaaaaaaaaa aaaaaaaaaa aaaggggggggg

```

870

(2) INFORMATION ON SEQ ID NO. 74:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1418 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

(2) INFORMATION ON SEQ ID NO. 76:

(A) LENGTH: 1712 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(A) ORGANISM: HUMAN
(C) ORGAN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```

gtggcagaaa acctcatgac acaatctctc cgcctccctg tgttggtgga ggatgtctgc 60
agcagcattt aaattctggg agggcttggg tgtcagcagc agcaggaggg gcagagcaca 120
gcatcgctcg gaccagactc gtctcaggcc agttgcagcc ttctcagcca aacgccgacc 180
aaggaaaact cactaccatg agaattgcag tgatttgctt ttgcctccta ggcatcacct 240
gtgccatacc agttaaacag gctgattctg gaagttctga ggaaaagcag ctttacaaca 300
aatacccaga tgctgtggcc acatggctaa accctgaccc atctcagaag cagaatctcc 360
tagccccaca gaatgctgtg tcctctgaag aaaccaatga ctttaaaca gagacccttc 420
caagtraagtc caacgaaagc catgaccaca tggatgatat ggatgatgaa gatgatgacg 480
accatgtgga cagccaggac tccattgact cgaacgactc tgatgatgta gatgacactg 540
atgattctca ccagtctgat gagtctcacc attctgatga atctgatgaa ctggctcactg 600

atcttccac ggacctgcca gcaaccgaag ttttccctc agttgtcccc acagtagaca 660
catatgatgg ccgagggtgat agtggtggtt atggactgag gtcaaaatct aagaagtttc 720
gcagacctga catccagtac cctgatgcta cagacgagga catcacctca cacatggaaa 780
gcgaggagtt gaatggtgca tacaaggcca tccccgttgc ccaggacctg aacgcgcctt 840
ctgattggga cagccgtggg aaggacagtt atgaaacgag tcagctggat gaccagagtg 900
ctgaaaccca cagccacaag cagtccagat tataaagcg gaaagccaat gatgagagca 960
atgagcattc cgatgtgatt gatagtcagg aactttccaa agtcagccgt gaattccaca 1020
gccatgaatt tcacagccat gaagatatgc tgggtgtaga cccaaaagt aaggaagaag 1080
ataaacacct gaaatttctg atttctcatg aattagatag tgcattctct gaggtcaatt 1140
aaaaggagaa aaaatacaat ttctcacttt gcatttagtc aaaagaaaa atgctttata 1200
gcaaaatgaa agagaacatg aaatgcttct ttctcagttt attggttgaa tgtgtatcta 1260
tttgagtctg gaaataacta atgtgtttga taattagttt agtttggtgg ttcattgaaa 1320
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actatcactg tattttaata ttgtttatc tctcatgaat agaaatttat gtagaagcaa 1440
acaaaatact ttaccact taaaagaga atataacatt ttatgtcact ataattcttt 1500
gttttttaag ttagtgata tttgttgtg attatctttt tgtggtgtga ataaatcttt 1560
tatcttgaat gtaataagaa ttggtgtgt tcaattgctt attgttttc ccacggtgt 1620
ccagcaatta ataaaacata accttttta ctgcctaaaa aaaaaaaga gaaaagaaaa 1680
aaaaaagaa aaaaaaagg gagggagggg ag
1712

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(2) INFORMATION ON SEQ ID NO. 78:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1273 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(A) LIBRARY: cDNA library

cgcgccccgc	ctgtgggtct	cagcagctcg	ggcggcggga	ggggtggcag	cggcaaggca	60
cccagtttc	gcgaaggctg	tcggcgcgcc	gcggcccgc	ggcaccgcgc	acgcgccttc	120
ccgcaggca	cccggcacgc	gccttccccg	ccgccacgat	gcccaagagg	aaggtcagct	180
cgcgccgaag	gccgccaaag	aagagcccaa	gaggagatcg	gcgcggttgt	cagctaaacc	240
cctgcaaaa	gtggaagcga	accgaaaaag	gcagcagcga	aggtaaatc	ttcagacaaa	300
aaagtgcaaa	caaaagggaa	aaggggagca	aagggaatac	aggccgaagt	ggctaaccaa	360
gaaactaaa	aagacttacc	tgcggaaaac	ggggaaacga	agactgagga	gagtccagcc	420
ctgatgaag	caggagagaa	agaagccaag	tctgattaat	aaccatatac	catgtcttat	480
cagtgggtccc	tgtctccctt	cttgtacaat	ccagaggaat	atttttatca	actattttgt	540
aaatgcaagt	tttttagtag	ctctagaaac	atttttaaga	aggaggaata	cccacctcat	600
cccatttttt	aagtgtaaat	gctttttttt	aagaggtgaa	atcatttgct	ggttggttat	660
cttttqgtac	aaccgaaaaa	tagtgtggga	tattgaatta	tgggaggctc	tgactgtctc	720

gggtgtcagc	ttaacattcc	acagatgggg	ggttagtttt	tatatcctat	aatacaaaagc	780
atattaaatg	gcaatatgga	gtcagtcctg	catttaatgt	cttgaacatt	ttaaattact	840
tctattacca	tgttgttttt	tagtagaatt	gtttcctaaa	gaaaaccact	ctttgtacct	900
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aataactttg	tctactgtgt	ctgaagaagt	acagatttga	acatgttagt	tacgtgtgtg	1020
tgagtgtgtg	actgttgggc	cgtatgtaac	agctgaccaa	cgtgaagata	ctgggtactg	1080
atagcctctt	aaggaaaaat	tgcttccaaa	ttttaagctg	gaaagtcact	ggaataactt	1140
taaaaaagaa	ttacaatatc	tggctcttta	gaatttcgtt	acgtatgtta	agatttgtgt	1200
acaaaattgaa	atgtctgtac	tgatcctcaa	ccaataaaat	ctcagttatg	aaaataaaaa	1260
aaaaaaaaaa	aaa					1273

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2342 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

```

ccctggacca ccggaactggc ctggggcggg acgtggggcg gggggcgcg cgtgcggcac 60
gctgcagggc tgaagcggcg gcggcggtgg ggactgcacg tagcccggcg ctcggcatgg 120
ctctcctggt gctcgggtctg gtgagctgta ccttctttct ggcaagtgaat ggtctgtatt 180
cctctagtga tgatgtgac gaattaactc catcaaattt caaccgagaa gttattcaga 240
gtgatagttt gtggcttgta gaattctatg ctccatgggtg tggtcactgt caaagattaa 300
caccagaatg gaagaaagca gcaactgcat taaaagatgt tgtcaaagt ggtgcagttg 360
atgcagataa gcatcattcc ctaggaggtc agtatgggtg tcagggattt cctaccatta 420
agatttttgg atccaacaaa aacagaccag aagattacca aggtggcaga actggtgaag 480
ccattgtaga tgctgcgctg agtgctctgc gccagctcgt gaaggatcgc ctcgggggac 540
gaagcggagg atacagttct ggaaaacaag gcagaagtga tagttcaagt aagaaggatg 600
tgattgagct gacagacgac agctttgata agaattgtct ggacagtga gattttgga 660
tggttgagtt ctatgctcct tgggtgggac actgcaaaaa cctagagcca gagtgggctg 720
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2342

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(i) SEQUENCE CHARACTERISTIC:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

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(2) INFORMATION ON SEQ ID NO. 81:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3708 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

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 taaacccgat aagcaacaaa aaccagacta acaaaatgtg taacaagaaa ctaatgacct 180
 ttctaaaatc aaacattcaa ttatctacaa tgtcttttta caaacgggga aaactccttg 240
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 ctgaagaaac tgaatcatta aaacagtaat tacgagttca caaattttaa acatttcaca 360
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(2) INFORMATION ON SEQ ID NO. 82:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3045 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

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(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) ANTI-SENSE: NO

(A) ORGANISM: HUMAN
(C) ORGAN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

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gaatgttaac caaaaaaaaaa aacagttgtg gtttttatte gctcttaaac tttgtgcatg 2760
ctttaacaat ttatcgcttt taaatctaga gtgaattcct aaagagctgc cgcta 2815

```

(2) INFORMATION ON SEQ ID NO. 84:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3462 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

ctggatcgta caagaaggga gacaaggacc actgacaaga taaggcctag caggaaacga 60
 agcggtctct tccgctatct gccgcttgtc caccggaagc gagttgcgac acggcaggtt 120
 cccgcccgga agaagcgacc aaagcgctg aggaccggca acatggtgcg gtcggggaat 180

aaggcagctg ttgtgctgtg tatggacgtg ggttttacca tgagtaactc cattcctggg 240
 atagaatccc catttgaaca agcaaagaag gtgataacca tgtttgtaca gcgacaggtg 300
 ttgctgaga acaaggatga gattgcttta gtctgtttg gtacagatgg cactgacaat 360
 cccctttctg gtggggatca gtatcagaac atcacagtgc acagacatct gatgctacca 420
 gattttgatt tgctggagga cattgaaagc aaaatccaac caggttctca acaggctgac 480
 ttcttggtg cactaatcgt gagcatggat gtgattcaac atgaaacaat agggaaagaag 540
 tttgagaaga ggcatattga aatattcact gacctcagca gccgattcag caaaagtgcg 600
 ctggatatta taattcatag cttgaagaaa tgtgacatct ccctgcaatt cttcttgcc 660
 ttctcacttg gcaaggaaga tggaggtggg gacagaggag atggccctt tcgcttaggt 720
 ggccatgggc cttcctttcc actaaaagga attaccgaac agcaaaaaga aggtcttgag 780
 atagtgaaaa tgggtgatgat atcttttaga ggtgaagatg ggttggtgaa aattttattca 840
 ttcatgaga gtctgagaaa actgtgcgtc ttcaagaaaa ttgagaggca ttccattcac 900
 tggccctgac gactgacctt tggctccaat ttgtctataa ggattgcagc ctataaatcg 960
 attctacagg agagagttta aaagacttgg acagttgtgg atgcaaaaac ctaaaaaaa 1020
 gaagatatac aaaaagaaac agttttattgc ttaaatgatg atgatgaaac tgaagtttta 1080
 aaagaggata ttattcaagg gtcccgctat ggaagtgata tagttccttt ctctaaagt 1140
 gatgaggaac aaatgaaata taaatcggag gggaggtgct tctctgtttt gggattttgt 1200
 aaatcttctc aggttcagag aagattcttc atgggaaatc aagttctaaa ggtctttgca 1260
 gcaagagatg atgagcgagc tgcagttgca ctttccctcc tgattcatgc tttggatgac 1320
 ttgacatgg tggccatagt tcgatatgct tatgacaaaa gagctaattc tcaagtcggc 1380
 gtggcttttc ctcatatcaa gcataactat gagtgtttag tgtatgtgca gctgcctttc 1440
 atggaagact tgcggcaata catgttttca tccctgaaaa acagtaagaa atatgtcccl 1500
 accgaggcac agttgaatgc tgttgatgct ttgattgact ccatgagctt ggcaaaagaaa 1560
 gatgagaaga cagacacctt tgaagaactt ttccaacca ccaaaatccc aaatcctcga 1620
 ttccaagatg tatttcagtg tctgtgcac agagctttac atccccggga gcctctaccc 1680
 ccaattcagc agcatatttg gaatatgctg aatcctcccg ctgaggtgac aacgaaaagt 1740
 cagattcctc tctctaaaat aaagaccctt tttcctctga ttgaagccaa gaaaaaggt 1800
 caagtgactg ctcaggaaat tttccaagac aacctgaag atggacctac agctaaaaaa 1860
 tttaaagact agcaaggggg agcccacttc agcgtctcca gtctggctga aggcagtgct 1920
 acctctgttg gaagtgtgaa tcttgctgaa aacttccgtg tctagtgaac acagaagaag 1980
 gccagctttg aggaagcgag taaccagctc ataaatcaca tcgaacagtt tttggatact 2040
 aatgaaacac cgtattttat gaagagcata gactgcattc gagccttccg ggaagaagcc 2100
 attaagtttt cagaagagca gcgctttaac aacttccctg aagcccttca agagaaagt 2160
 gaaattaaac aattaaatca tttctgggaa attgttgctc aggatggaat tactctgac 2220
 cccaaagagg aagcctctgg aagttctgtc acagctgagg aagccaaaaa gtttctggcc 2280
 cccaaagaca aaccaagtg agacacagca gctgtatttg aagaaggtgg tgatgtggac 2340
 gatttatttg acatgatata ggtcgtggat gtatggggaa tctaagagag ctgccatcgc 2400
 tgtgatgctg ggagttctaa caaaacaagt tggatgcggc cattcaaggg gagccaaaat 2460
 ctcaagaaat tcccagcagg ttacctggag gcgcatcac taattctctg tggaaatga 2520
 acacacatat atattacaag ggataattta gacccatac aagtttataa agagtcattg 2580
 ttattttctg gttgggtgat tattttttct gtggtcttac tgatctttgt atattacata 2640
 catgctttga agtttctgga aagtagatct tttcttgacc tagtatatca gtgacagttg 2700
 cagcccttgt gatgtgatta gtgtctcatg tggaaacctg gcatggttat tgatgagttt 2760
 cttaaccctt tccagagtc tcttttgcc gatcctccaa cagctgtcac aacttgtggt 2820
 gagcaagcag tagcatttgc ttcttcccaa caagcagctg ggttaggaaa acctgggta 2880
 aggacggact cacttctct tttagttgag gccttctagt taccacatta ctctgcccct 2940
 gtatataggt ggttttctt aagtgggggt ggaaggggag cacaatttcc cttcatactc 3000
 cttttaagca gtgagttatg gtggtggtct catgaagaaa agacctttt gcccaatctc 3060
 tgccatatca gtgaacctt agaaactcaa aaactgagaa atttactaca gtatgtagaa 3120
 ttatatcact tcaactgttct ctacttgcaa gcctcaaaga gagaaagttt cgttatatta 3180
 aaacactttg ttaacttttc ggtctttccc atttctacct aagtcagctt tcatctttgt 3240
 ggatggtgtc tcttttacta aataagaaaa cttattctct tttttcttg 3300
 tctcattct tgccttgagt tccagttcct ctttggtgta cagacttctt ggtaccaggt 3360
 cactctgtc ttcagcacc tcataagtcg tctaataac acagttttgt acatgtaaca 3420
 ttaaaggcat aaatgactca aaaaaaaaaa aaaaaaaaaa aa 3462

(2) INFORMATION ON SEQ ID NO. 85:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 668 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

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atagggccgg tgctgcctgc ggaagccggc ggctgagagg cagcgaactc atctttgcc 60
gtacaggagc tcgtgccgtg gcccacagcc cacagcccac agccatgggc tgggacctga120
cggtgaagat gctggcgggc aacgaattcc aggtgtccct gagcagctcc atgtcgggtgt180
cagagctgaa ggcgcagatc acccagaaga tcggcgtgca cgccttcag cagcgtctgg240
ctgtccaccc gagcgggtgtg gcgctgcagg acagggtccc ccttgccagc cagggcctgg300
gccccggcag cacgggtcctg ctggtgggtgg acaaatgcga cgaacctctg agcatcctgg360
tgaggaataa caagggccgc agcagcacct acgaggtgcg gctgacgcag accgtggccc420
acctgaagca gcaagtgagc gggctggagg gtgtgcagga cgacctgttc tggctgacct480
tcgaggggaa gccctggag gaccagctcc cgctggggga gtacggcctc aagcccctga540
gcaccgtgtt catgaatctg cgcctgcggg gaggcggcac agagcctggc gggcggagct600
aagggcctcc accagcatcc gagcaggatc aagggccgga aataaaggct gttgtaaaaga660
gaaaaaaa

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668

(2) INFORMATION ON SEQ ID NO. 86:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 671 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

(2) INFORMATION ON SEQ ID NO. 88:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1108 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

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agtggaggag ggagagacgc tggcccggga cccgaggggc gtgggcatcg ggaggcgggc 60
ccgggttagg ggcgggaccg ccgcctggtt aaaggcgctt atttcccagg cagccgctgc 120
agtcgccaca cctttgcccc tgetgcgatg accctgtcgc cacttctgct tcggacgtcc 180
ccacggcggc ggtgcaggcg tcccctctgc aagcgttaga cttctttggg aatggggcac 240
cagttaacta caagacaggc aatctatacc tgcggggggc cctgaagaag tccaatgcac 300
cgcttgctaa tgtgaccctc tactatgaag cactgtgcgg tggctgccga gccttcctga 360
tccgggagct cttcccaaca tggctgttgg tcatggagat cctcaatgtc acgctgggtg 420
cctacggaaa cgcacaggaa caaaatgtca gtggcagggt ggagttcaag tgccagcatg 480
gagaagagga gtgcaaattc aacaagggtg aggcctgcgt gttggatgaa cttgacatgg 540
agctagcctt cctgaccatt gtctgcatgg aagagtttga ggacatggag agaagtctgc 600
cactatgcct gcagctctac gccccagggc tgtcgccaga cactatcatg gagtgtgcaa 660
tgggggaccg cggcatgcag ctcatgcacg ccaacgcccc gcggacagat gctctccagc 720
caccgcacga gtatgtgccc tgggtcaccg tcaatgggaa acccttgga gatcagacc 780
agtcctttac ccttgtctgc cagttgtacc agggcaagaa gccggatgtc tgcccttcc 840

caaccagctc cctcaggagt gtttgcttca agtgatggcc ggtgagctgc ggagagctca 900
tggaaggcga gtgggaaccc ggctgcctgc cttttttct gatccagacc ctgggcacct 960
gttacttacc aactggaaaa ttttatgcat cccatgaagc ccagatacac aaaattccac 1020
cccatgatca agaatcctgc tccactaaga atggtgctaa agtaaaacta gtttaataag 1080
ccccaaaaaa aaaaccgcgt cggtcgac 1108

```

(2) INFORMATION ON SEQ ID NO. 89:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 720 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```

aaagcagccg cggcgccgg gtgcctcaca gcacgctgcc acgcccagcg agacccctct 60
ctgcacgcca gcccgccgc acccaccatg gccacagttc agcagctgga aggaagatgg120
cgccctgggg acagcaaagg ctttgatgaa tacatgaagg agctaggagt gggaatagct180
ttgcgaaaaa tgggcgcaat ggccaagcca gattgtatca tcacttgta tggtaaaaaac240
ctcaccataa aaactgagag cactttgaaa acaacacagt tttctgtac cctgggagag300
aagtttgaag aaaccacagc tgatggcaga aaaactcaga ctgtctgcaa ctttacagat360
ggtgcattgg ttcagcatca ggagtgggat gggaaggaaa gcacaataac aagaaaattg420
aaagatggga aattagtggg ggagtgtgtc atgaacaatg tcacctgtac tcggatctat480
gaaaaagtag aataaaaaatt ccatacatcac tttggacagg agttaattaa gagaatgacc540
aagctcagtt caatgagcaa atctccatac tgtttctttc tttttttttt cattactgtg600
ttcaattatc tttatcataa acattttaca tgcagctatt tcaaagtgtg ttggattaat660
taggatcacc cctttggtta ataaataaat gtgtttgtgc taaaaaaaaa aaaaaaaaaa720

```

(2) INFORMATION ON SEQ ID NO. 90:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 837 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```

ctctcgcgag gattggctgt tagcggcggt gtagttaagc tcgtgtaacg gcggcggtgt 60
cggcagctgc tgtagcgaag agagtttggc gcgatgtctc acaccatttt gctggtacag120
cctaccaaga ggccagaagg cagaacttat gctgactacg aatctgtgaa tgaatgcatg180
gaagggtgtt gtaaaatgta tgaagaacat ctgaaaagaa tgaatcccaa cagtcctct240
atcacatatg acatcagtca gttgtttgat ttcacgatg atctggcaga cctcagctgc300
ctgggtttacc gagctgatac ccagacatac cagccttata acaaagactg gattaaagag360
aagatctacg tgctccttcg tcggcaggcc caacaggctg ggaaataatt gtgttggaa420
cactgggggg gttgggggtg gcttggaaca caggtgtgta cagcgtgctg tagtggaa480
tttgtatcat agtaatcctg tttccacttt gttatactct agccaagatt gactgtatta540
gatgaaatgt gaggatcttg ttcaatcgga aacccccgtt acctcctctt tttctttctc600
tttctttttt ttttttact taaacatttt tatgatgatt tagatggaag ttgttcttcg660
tcacttaatg ttgggtccag tccttcaact gttcatactc actttataac attcacatac720
taacccttct tcaagatggg gtgggggggtg gaaatgcagt ttagccatgt cctcaagata780
aagtccttgg aaaaaataat aaatgtcctt tagttataaa aaaaaaaaaa aaaaaaa 837

```

(2) INFORMATION ON SEQ ID NO. 91:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 498 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```

gtagggtcag cgtcggaggc ggtagtgcag gtggcggttc cttgagggaag agtgaggggtt 60
ccaaacttttc tgcttatctg ggaggtgttg ggcgcggaca gtcgagatgt cagagaaaaa120
gcagccggta gacttaggtc tgtagagga agacgacgag ttgaagagt tccctgccga180
agactgggct ggcttagatg aagatgaaga tgcacatgtc tgggaggata attgggatga240
tgacaatgta gaggatgact tctcaatca gttacgagct gaactagaga aacatgggta300
taagatggag acttcatagc atccagaaga agtgttgaag taacctaaac ttgacctgct360
taatacattc tagggcagag aaccaggat gggacactaa aaaaatgtgt ttatttcatt420
acctgcttgg atttatttgt gtttttgtaa cacaaaaaat aaatgttttg atataaaaag480
gaaagagaaa aattgcgg                                     498

```

(2) INFORMATION ON SEQ ID NO. 92:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1077 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

cggctcgagc tgggtacaaca gggcacacgt gtttcacggt gacagggttg cttggggacgc 60
tagtaaccat gggcttgctg acttagccaa agaagagtta agaagaaaat acacacaagt 120
atacagactg ttcttagttt cttagactta tctgcatatt ggataaaaata aatgcaattg 180
tgctcttcat ttaggatgct ttcattgtct ttaagatgtg ttaggaatgt caacagagca 240
aggagaaaaa aggcagtcct ggaatcacat tcttagcaca cctacacctc ttgaaaatag 300
aacaacttgc agaattgaga gtgattcctt tcctaaaagt gtaagaaagc atagagattt 360
gttcgtattt agaatgggat cacgaggaaa agagaaggaa agtgattttt ttccacaaga 420
tctgtaatgt tatttccact tataaaggaa ataaaaaatg aaaaacatta tttggatata 480
aaaagcaaat aaaaacccaa ttcagtctct tctaagcaaa attgctaaag agagatgaac 540
cacattataa agtaatcttt ggctgtaagg cattttcatc tttccttcgg gttggcaaaa 600
tattttaaag gtaaaacatg ctggtgaacc aggggtgttg atggtgataa gggaggaata 660
tagaatgaaa gactgaatct tcctttgttg cacaaataga gtttgaaaaa agcctgtgaa 720
aggtgtcttc tttgacttaa tgtctttaa agtatccaga gatactacaa tattaacata 780
agaaaagatt atatattatt tctgaatcga gatgtccata gtcaaatttg taaatcttat 840
tcttttgtaa tatttattta tatttattta tgacagttaa cattctgatt ttacatgtaa 900
aacaagaaaa gttgaagaag atatgtgaag aaaaatgtat ttttcctaaa tagaaataaa 960
tgatcccatt ttttggtaaa aaaaagtatg tgagatttat tcgtaaactg gactacttta 1020
tttctaaata agagattccc tacctgcgtc ctacaagcag ttcagaatgc catgcct 1077

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(2) INFORMATION ON SEQ ID NO. 93:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1755 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

gcagaggctg	cttgtgatct	ggtacgagga	tatatcaagt	tttttgaggg	acctgtgaca	60
ggaatcttct	ctggttatgt	taattccatg	ctgcaggaat	acgcaaaaaa	tccatctgtc	120
aactggaaac	acaaagatgc	agccatctac	ctagtgcacat	ctttggcatc	aaaagcccaa	180
acacagaagc	atggaattac	acaagcaaat	gaacttgtaa	acctaactga	gttcttttgt	240
aatcacatcc	ccctgatatt	aaaatcagct	aatgtgaatg	aatttctgtt	ctctaaagct	300
gacggtatca	tacattattat	gatttttaga	aatcaagtgc	caaaagaaca	tcttttagtc	360
tcgattcctc	tcttgattaa	tcatcttcaa	gctgaaagta	ttgttgttca	tacttacgca	420
gctcatgctc	ttgaacggct	ctttactatg	cgagggccta	acaattgccac	tctctttaca	480
gctgcagaaa	ctgcacggtt	tgttgagatt	ctgtcaacaa	accttttcaa	agctctcaca	540
cttcttggtc	tctcagaaaa	tgaatatatt	atgaaagcta	tcatgagaag	tttttctctc	600
ctacaagaag	ccataatccc	ctacatccct	actctcatca	ctcagcttac	acagaagcta	660
ttagctgtta	gtaagaaccc	aagcaaacct	cactttaatc	actacatggt	tgaagcaata	720
tgtttatcca	taagaataac	ttgcaaagct	aaccctgctg	ctggttgtaa	ttttgaggag	780
gctttgtttt	tggtgtttac	tgaatatctta	caaaatgatg	tgcagaagatt	tattccatac	840
gtctttcaag	tgatgtcttt	gcttctggaa	acacacaaaa	atgacatccc	gtcttcctat	900
atggccttat	ttctctatct	ccttcagcca	gtgctttggg	aaagaacagg	aaatattcct	960
gctctagtga	ggcttcttca	agcattctta	gaacgcggtt	caaacacaat	agcaagtgct	1020
gcagctgaca	aaattcctgt	gttactaggt	gtctttcaga	agctgatgtc	atccaaagcal	1080
aatgaccacc	aaggttttga	tcttctaaac	agtataatag	agcacattgc	tccgaaatcal	1140
gttgaccaat	ataggaaaca	aatcttctatt	ctgctattcc	agagacttca	gaattccaaa	1200
acaaccaagt	ttatcaagag	ttttttagtc	tttattaatt	tgtattgcat	aaaatatggg	1260
gcactagcac	tacaagaaat	atttgatggt	atacaaccaa	aaatgtttgg	aatggttttg	1320
gaaaaaatta	ttattcctga	aattcagaa	gtatctggaa	atgtagagaa	aaagatctgt	1380
gcggttgcca	taaccaaatt	actaacagaa	tgtcccccac	tgatggacac	tgagtatacc	1440
aaactgtgga	ctccattatt	acagtctttg	attggtcttt	tgtagttacc	cgaagatgat	1500
accattcctg	atgaggaaca	ttttattgac	atagaagata	caccaggata	tcagactgcc	1560
ttctcacagt	tggcatttgc	tgggaaaaaa	gagcatgatc	ctgtaggtca	aatggtgaat	1620
aaccccaaaa	ttcacctggc	acagtcactt	cacaagttgt	ctaccgcctg	tccaggaagg	1680
gttccatcaa	tggcaaaaga	ctctgtgata	aatggagact	ttaatgggag	ggcaaaagga	1740
taataagtgt	tctgg					1755

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1545 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

gttcggcgag cgagcacctt cgacgcggtc cggggacccc tcgtcgctgt cctcccgcag 60
cggaccctgg gccccaggct cgcgctgccc ggcagggtgc tcgtgtccca cctccggcgc 120
acgcctcccg cgagtcocgg gccctcccg cgcctctctt ctgcgcgcgc gcgcagatcg 180
gcgccccgcg aggtccctgc gttcgggctt ctgcttgccg cggcgacggc gacttttgcc 240
gcagctcagg aagaatgtgt ctgtgaaaac tacaagctgg ccgtaaactg ctttgtgaat 300
aataatcgtc aatgccagtg tacttcagtt ggtgcacaaa atactgtcat ttgctcaaag 360
ctggctgcca aatgtttggt gatgaaggca gaaatgaatg gctcaaaact tgggagaaga 420
gcaaaacctg aaggggccct ccagaacaat gatgggcttt atgatcctga ctgcgatgag 480
agcgggctct ttaaggccaa gcagtgaac ggcacctcca tgtgctggtg tgtgaacact 540
gctgggggtca gaagaacaga caaggacact gaaataacct gctctgagcg agtgagaacc 600
tactggatca tcattgaact aaaacacaaa gcaagagaaa aaccttatga tagtaaaagt 660
ttgcggactg cacttcagaa ggagatcaca acgcgttatc aactggatcc aaaatttatc 720
acgagttatt tgtatgagaa taatgtttatc actattgatc tggttcaaaa ttcttctcaa 780
aaaactcaga atgatgtgga catagctgat gtggcttatt attttgaaaa agatgttaaa 840
ggtgaatcct tgtttcattc taagaaaatg gacctgacag taaatgggga acaactggat 900
ctggatcctg gtcaaaactt aattttattat gttgatgaaa aagcacctga attctcaatg 960
caggggtctaa aagctgggtg tattgctggt attgtggttg tggatagc agttgttgct 1020
ggaattgttg tgctggttat ttccagaaaag aagagaatgg caaagtatga gaaggctgag 1080
ataaaggaga tgggtgagat gcatagggaa ctcaatgcat aactatataa tttgaagatt 1140
atagaagaag ggaaatagca aatggacaca aattacaaat gtgtgtgcgt gggacgaaga 1200
catctttgaa ggtcatgagt ttgttagttt aacatcatat atttgtaata gtgaaacctg 1260
tactcaaaat ataagcagct tgaaactggc ttaccaatc ttgaaatttg accacaagtg 1320
tcttatatat gcagatctaa tgtaaaatcc agaacttga ctccatcggt aaaattattt 1380
atgtgtaaca ttcaaagtgt tgcattaaat atgcttcac agtaaaatct gaaaaactga 1440
tttgtgattg aaagctgcct ttctatttac ttgagctctg tacatacata cttttttatg 1500
agctatgaaa taaaacattt taaactgaaa aaaaaaaaaa aaggc 1545

```

(2) INFORMATION ON SEQ ID NO. 95:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1133 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```

gagcggtatt atcgggtaga catctcgac cgcgtctcgg aaaccggtag cgcttgacgc 60
atggctgacc aactgactga agagcagatt gcagaattca aagaagcttt ttcactatct 120
gacaaagatg gtgatggaac tataacaaca aaggaattgg gaactgtaat gagatctctt 180
gggcagaatc ccacagaagc agagttacag gacatgatta atgaagtaga tgctgatggt 240
aatggcacia ttgaacttcc ctgaatttct ggacaaggat ggcaagaaaa atgaaagaca 300
cagacagtga agaagaaatg agagaagcat tccgtgtgtt tgataaggat ggcaagggct 360
atatgagtgc tgcagaactt cgccatgtga tgacaaacct tggagagaag ttaacagatg 420
aagaagttga tgaatgatc agggaaagcag atattgatgg tgatgggtcaa gtaaaactatg 480
aagagtttgt acaaagtgtg acagcaaagt gaagaccttg tacagaatgt gttaaatttc 540
ttgtacaaaa ttgtttatct gccctttctt tgtttgtaac ttatctgtaa aagggtttctc 600
cctactgtca aaaaaatatg catgtatagt aattaggact tcattcctcc atgttttctt 660
cccttatctt actgtcattg tcctaaaaac ttattttaga aaagttgatc aaggtaacat 720
gttgcatgtg gcttactctg gggaaatatc taagcccttc tgcacatcta aacttagatg 780
gagttgggtc aatgagggaa catctgggtt atgccttttt taaagtagtt ttcttttagga 840
actgtcagca tgttggtgtt gaagtgtgga gttgtaactc tgcgtggact atggacagtc 900
aacaatatgt acttaaaagt tgcactattg caaaacgggt gtattatcca ggtactcgta 960
cactatcttt ttgtactgct ggtcctgtac cagaaacatt ttcttttatt gttacttgct 1020
ttttaaactt gggttagcca cttaaaatct gcttatggca caatttgccc caaaatccat 1080
tccaagttgt atatttggtt tccaataaaa aaattacaat ttacccaaaa aaa 1133

```

(2) INFORMATION ON SEQ ID NO. 96:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 791 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

```

gccgcccgcg cggaccgcgc gagaggcgcc ggccgggagcg gcggtgatgg acgggtccgg 60
ggagcagccc agaggcgggg ggcccaccag ctctgagcag atcatgaaga caggggccct120
tttgcttcag ggtttcatcc aggatcgagc agggcggaatg gggggggagg caccgagct180
ggccctggac ccggtgcctc aggatgctgc caccaagaag ctgagcgaat gtctcaagcg240
catcggggac gaactggaca gtaacatgga gctgcagagg atgattgccg ccgtggacac300
agactccccc cgagaggtct tttccgagt ggcagctgac atgtttctg acggcaactt360
caactggggc cgggttgctg ccttttcta ctttgccagc aaactgggtc tcaaggccct420
gtgcaccaag gtgccggaac tgatcagaac catcatgggc tggacattgg acttcctccg480
ggagcggctg ttgggctgga tccaagacca gggtggttgg gacggcctcc tctcctactt540
tgggacgccc acgtggcaga ccgtgaccat ctttgtggcg ggagtgtca ccgcctcact600
caccatctgg aagaagatgg gctgaggccc ccagctgcct tggactgtgt tttcctcca660
taaattatgg catttttctg ggagggtg ggattggggg acatgggcat tttcttact720
tttgtaatta ttggggggtg tggggaagag tggctctgag ggggtaataa acctccttcg780
ggacacaaaa a

```

791

(2) INFORMATION ON SEQ ID NO. 97:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 599 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

```

tcttgccttc accatgaagt ccagcggcct ctcccccctc ctggtgctgc ttgccctggg 60
aactctggca ccttgggctg tggaaaggctc tggaaagtcc ttcaaagctg gagtctgtcc120

tcttaagaaa tctgcccagt gccttagata caagaaacct gagtgcaga gtgactggca180
gtgtccaggg aagaagagat gttgtcctga cacttggtgc atcaaatgcc tggatcctgt240
tgacacccca aacccaacaa ggagggaagc tgggaagtgc ccagtgaact atggccaatg300
tttgatgctt aaccccccca atttctgtga gatggatggc cagtgcgaagc gtgacttgaa360
gtgttgcatg ggcattgtgt ggaaatcctg cgtttccccc gtgaaagctt gattcctgcc420
atatggagga ggctctggag tctgtctctg tgtgggtccag gtcccttcca ccttgagact480
tggctccacc actgatatac tcttttgggg aaaggcttgg cacacagcag gctttcaaga540
agtgcagtt gatcaatgaa taaataaacg agcctatttc tctttgcaaa aaaaaaaaaa 599

```

(2) INFORMATION ON SEQ ID NO. 98:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 643 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

```

gggcccgcgg ctcgggcgta ggaggcggtg cctctgcagc aagcgtgggg cgcggaacc 60
cgagcaggac tctccagtc tcagtcacct tggacaaaga agtgtggatc ctcagattcc120
atcttttcca actccaaggt gccatggcag agaaggtgct ggtaacaggt ggggctggct180
acattggcag ccacacggtg ctggagctgc tggaggctgg ctacttgctt gtggatcatc240
ataacttcca taatgccttc cgtggagggg gctccctgcc tgagagcctg cggcgggtcc300
aggagctgac aggccgctct gtggagtgtg aggagatgga cattttggac caggagagccc360
tacagcgtct cttcaaaaag tacagcttta tggcggtcat ccactttgcy gggctcaagg420
ccgtgggcga gtcggtgcag aagcctctgg attattacag agttaacctg accgggacca480
tccagcttct ggagatcatg aaggccacg gggatgaaga cctggtgttc agcagctcag540
ccactgtgta cgggaacccc cagtacctgc ccccttgaat gagggccacc ccacgggggtg600
ggatgtaaca accttacgga agtccaaatt tctttatctt ttc 643

```

(2) INFORMATION ON SEQ ID NO. 99:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 860 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

ctcgagccgc tcgagccgat tcggctcgag tgccctccaga ggactggcca cttttgcct 60
agataaagat gcacttagag atgaatatga tgatctctca gatttgaatg cagtacaaat120
ggagagtgtt cgagaatggg aaatgcagtt taaagaaaaa tatgattatg taggcagact180
cctaaaacca ggagaagaac catcagaata tacagatgaa gaagatacca aggatcacaa240
taaacaggat tgaactttgt aaacaaccaa agtcaggggc cttcagaact gcaattctta300
ctccctttca cagactgtcc ggagtctttg ggtttgattc acctgctgcg aaaaacattc360
aacaaattgt gtacaagata aattaatctc actatgaaga tttgaataac tagacattat420
ttatgctgcc aaactcattt gttgcagttg tttgtaatgt ctagtggggc ttcacatcc480
tgaaaagaag gagacaggga tttttttaa gacaaagaaa gtcacaatat tacttctttc540
cttccttttt tctctctttc ctttcttctt tctctttctt tctttttaa atatttgaa600
gacaaccaga tatgtatttg ctactcaagt gtacagatct cctcaagaaa catcaaggga660
ctcctgtgtc acatactgtg tttttatttt aacatgggtg agggaggcga cctgatcagg720
ggaggtgggg gtacacatca atttgagttg ttcaggctac tgaaacatta aaatgtgaat780
tcccaaactt ttctttttgg cattgttcgg gggataggga aatatcgtt ttaaaggagt840
cttggaatt gggtgtggga                                     860

```

(2) INFORMATION ON SEQ ID NO. 100:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```

ggggggtcgc ccagcctggc ccgggggagag gactggctgg gcagggggcgc cggcccgcc 60
cgggagagggc gggccggggcg gggctgggag tatttgaggc tcggagccac cggcccgcc 120
gcggcccgag caccctcctcg ccagcagccg tccggagcca gccaacgagc ggaaaaatggc 180
agacaatttt tcgctccatg atgcgttatc tgggtctgga aaccctaaacc ctcaaggatg 240
gcctggcgca tgggggaacc agcctgctgg ggcagggggc taccagggg ctccctatcc 300
tggggcctac cccgggcagg caccctcagg ggcttatcct ggacaggcac ctccagggcg 360
ctaccctgga gcacctggag cttatcccg agcacctgca cctggagtct acccagggcg 420
accagcgggc cctggggcct acccatcttc tggacagcca agtggcaccg gagcctaccc 480
tgccactggc ccctatggcg cccctgctgg gccactgatt gtgcctata acctgccttt 540
gcctggggga gtggtgcctc gcatgctgat aacaattctg ggcacggtga agcccaatgc 600
aaacagaatt gcttttagatt tccaaagagg gaatgatgtt gccttccact ttaaccacg 660
cttcaatgag aacaacagga gagtcatgtt ttgcaatata aagctggata ataactgggg 720
aaagggaagaa agacagtcgg ttttccatt tgaaagtggg aaaccattca aaatacaagt 780
actggttga cctgaccact tcaagggtgc agtgaatgat gctcacttgt tgcagtacaa 840
tcctcgggtt aaaaaactca atgaaatcag caaactggga atttctggtg acatagacct 900
taccagtgtc tcataatacca tgatataatc tgaaaggggc agattaaaaa aaaaaaaaga 960
atctaaacct tacatgtgta aagggttcat gttcactgtg agtgaaaatt tttacattca 1020
tcaatatccc tcttgtaagt catctactta ataaatatta cagtgaaaaa aaaaaaaaaa 1080
aaaaaaaaaa gtcgaaaaag gagggggaag gagagagagg gaagaagaga gaggagaagg 1140
aggggggggg tgggt 1155

```

(2) INFORMATION ON SEQ ID NO. 101:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 522 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

aaaaatattt gctggaaatt gctgtgtagg attacaggcg tgaccactgc gcccgggcac 60
attcagttct tatcaaagaa ataaccaga cttaatcttg aatgatacga ttatgcccac 120
tattaagtaa aaaatataag aaaaggttat cttaaataga tcttaggcaa aataccagct 180
gatgaaggca tctgatgcct tcatctgttc agtcatctcc aaaaacagta aaaataacca 240
ctttttgttg ggcaatatga aatttttaaa ggagtagaat accaaatgat agaaacagac 300
tgctgaatt gagaattttg atttcttaaa gtgtgtttct ttctaaattg ctgttcctta 360

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atttgattaa ttttaattcat gtattatgat taaatctgag gcagatgagc ttacaagtat420
tgaaataaatt actaattaat cacaaatgtg aagttatgca tgatgtaaaa aatacaaaaca480
ttctaattaa aggcctttgca acacaaaaaa aaqaaaaaaa aa 522

```

(2) INFORMATION ON SEQ ID NO. 102:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1628 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```

ccagctcgcc ctgcctagcc agggggcgccc cgccccctgc ctgcccggcc accttcggga 60
gccgcttcca ataggcgcttc gccattggct ctggcgacct ccgcgcgttg ggaggtgtag 120
cgcggtcttg aacgcgctga gggccgttga gtgtcgacagg cggcgagggc gcgagtgagg 180
agcagaccca ggcctcgccg gccgagaagg ccggggcgctc ccacactgaa ggtccggaaa 240
ggcgacttcc gggggctttg gcacctggcg gacctcccg gagcgtcggc acctgaacgc 300
gaggcgctcc attgcgcgtg cgcgttgagg ggcttcccgc acctgatcg gagacccaa 360
cggctggttg cgtgcctgc gcgtctcgcc tgagctggcc atggcgagc gtgcccgtg 420
aggcggagcg ggcgtttctc gccctgctgg gatcgctgct cctctctggg gtcctggcg 480
ccgaccgaga acgcagcacc cagcattct gcctgggtgc gaaggtggtg ggcagatgcc 540
gggcctccat gcctaggttg tggtaaatg tcactgacgg atcctgccag ctggttgtgt 600
atgggggctg tgacggaaac agcaataatt acctgaccaa ggaggagtgc ctcaagaaat 660
gtgccactgt cacagagaat gccacgggtg acctggccac cagcaggaat gcagcggatt 720
cctctgtccc aagtgtccc agaaggcagg attctgaaga ccactccagc gatatgttca 780
actatgaaga atactgcacc gccaacgcag tcactgggcc ttgccgtgca tccttcccac 840
gctggtactt tgacgtggag aggaactcct gcaataaact catctatgga ggctgccggg 900
gcaataagaa cagctaccgc tctgaggagg cctgcatgct ccgctgcttc cgccagcagg 960
agaatcctcc cctgccccct ggctcaaagg tggtggttct ggcggggctg ttcgtgatgg 1020
tggtgatcct cttcctggga gcctccatgg tctacctgat ccgggtggca cggaggaacc 1080
aggagcgtgc cctgcgcacc gtctggagct ccggagatga caaggagcag ctggtgaaga 1140
acacatatgt cctgtgaccg ccctgtcgcc aagaggactg gggaagggag gggagactat 1200
gtgtgagctt tttttaaata gagggattga ctcgatttg agtgatcatt agggctgagg 1260
tctgtttctc tgggaggtag gacggctgct tccgtgtctg gcagggatgg gtttgccttg 1320
gaaatcctct aggagctcc tccctgcagt gcctgcagtc tggcagcagc cccgagttgt 1380
ttcctcgctg atcgatttct ttccctccagg tagagtttct tttgcttatg ttgaattcca 1440
ttgctctttt tctcatcaca gaagtgatgt tggaatcggt tcttttgttt gtctgattta 1500
tggttttttt aagtataaac aaaagttttt tattagcatt ctgaaagaag gaaagtaaaa 1560
tgtacaagtt taataaaaag gggccttccc ctttagaata aaaaaaaaaa aaaaaaaaaa 1620
aaaaaaaaa

```

(2) INFORMATION ON SEQ ID NO. 103:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 605 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

cctggcagct gtcggctgga aggaactggt ctgctcacac ttgctggctt gcgcatcagg 60
actggcttta tctcctgact cacggtgcaa aggtgcactc tgcgaacggt aagtccgtcc120
ccagcgcttg gaatcctacg gccccacag cgggatcccc tcagccttcc aggtcctcaal80
ctcccgcgga cgtcgaacaa tggcctccat ggggctacag gtaatgggca tcgcgctggc240
cgtcctgggc tggctggccg tcatgctgtg ctgcgcgctg cccatgtggc gcgtgacggc300
cttcacggc agcaacattg tcacctcgca gaccatctgg gagggcctat ggatgaactg360
cgtggtgcag agcaccggcc agatgcagtg caagggtgtac gactcgctgc tggcactgcc420
gcaggacctg caggcggccc gcgccctcgt catcatcagc atcatcgtgg ctgctctggg480
cgtgctgctg tccgtgggtg ggggcgaagt gtaacaaact tgcctggagg attaaaagcg540
ccaagggcaa gaacatgatt cgttggcggg cgtgggtgtt tctgtttggg ccggcctaata600
gggtg

```

605

(2) INFORMATION ON SEQ ID NO. 105:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2731 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

agggggggcgg acagacacag actatgcaga tgggagtgaa gacaaagtag tagaagtagc 60
agaggaggaa gaagtggctg aggtggagga cgatgaggat ggtgatgagg tagaggaaga 120
ggctgaggaa ccctacgaag aagccacaga gagacacaga gtctgtggaa gaggtgggtc 180
gagagggtgtg ctctgaacaa gccgagacgg ggccgtgccg agcaatgatc tcccgctggg 240
actttgatgt gactgaaggg aagtgtgccc cattctttta cggcggatgt ggcggcaacc 300
ggaacaactt tgacacagaa gactactgca tggccgtgtg tggcagcgcc attcctacaa 360
cagcagccag taccctgat gccgttgaca agtatctcga gacacctggg gatgagaatg 420
aacatgcccc tttccagaaa gccaaagaga ggcttgaggc caagcaccga gagagaatgt 480
cccaggteat gagagaatgg gaagaggcag aacgtcaagc aaagaacttg cctaaagctg 540
ataagaaggc agttatccag catttccagg agaaagtggg atctttggaa caggaagcag 600
ccaacgagag acagcagctg gtggagacac acatggccag agtggaagcc atgctcaatg 660
accgcgcgcg cctggccctg gagaactaca tcaccgctct gcaggctgtt cctcctcggc 720
ctcgtcacgt gttcaatatg ctaaagaagt atgtccgcgc agaacagaaq gacagacagc 780
acaccctaaa gcatttcgag catgtgcgca tgggtgatcc caagaaagcc gctcagatcc 840
ggtcccagggt tatgacacac ctccgtgtga tttatgagcg catgaatcag tctctctccc 900
tgcttcaaaa cgtgcctgca gtggcggagg agattcagga tgaagttagt gagctgcttc 960
agaaagagca aaactattca gatgacgtct tggccaacat gattagttaa ccaaggatcal 1020
gttacggaaa cgatgctctc atgccatctt tgaccgaaac gaaaaccacc gtggagctcc 1080
ttcccgtaga tggagagttc agcctggacg atctccagcc gtggcattct tttggggctg 1140
actctgtgcc agccaacaca gaaaacgaag ttgagcctgt tgatgcccgc cctgctgccg 1200
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aattggtgtt ctttgcagaa gatgtgggtt caaacaaggg tgcaatcatt ggactcatgg 1380
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agtacacatc cattcatcat ggtgtggtag aggttgacgc cgctgtcacc ccagaggagc 1500
gccacctgtc caagatgcag cagaacggct acgaaaatcc aacctacaag ttctttgagc 1560
agatgcagaa ctagaccccc gccacagcag cctctgaagt tggacagcaa aaccattgct 1620
tcaactacca tcggtgtcca tttatagaat aatgtgggaa gaaacaaacc cgttttatga 1680
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tattaatggg ttttgtgtac tgtaagaat ttagctgtat caaactagtg catgaataga 1860
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gaacgtggga gttcagctgc ttctcttgcc taagtattcc ttctctgate actatgcatt 2040
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caattttctt taaccagctc gaagtttcat ttatgataca aaagaagatg aaaatggaag 2580
tggcaatata aggggatgag gaaggcatgc ctggacaaac ccttctttta agatgtgtct 2640
tcaatttgta taaaatgggt ttttcatgta aataaataca ttcttgaggg agccaaaaaa 2700
aactatatta ctggcaggtt tataatatgg c 2731

```

(2) INFORMATION ON SEQ ID NO. 106:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2194 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```

gaattcagaa gttaatgatg ttgggtaaga gaacaatggt aagagagcaa tctaagaata 60
tatcacctac ttaatttta tatgagagta catggaggta gctgtgatgt ggaaatgtag 120
cactgctcct acccacgcag atttattcca gtgaaacaac aactggaact tcaagtaact 180
cctcccagag tacttccaac tctgggttgg ccccaaatcc aactaatgcc accaccaagg 240
cggctgggtg tgccctgcag tcaacagcca gtctcttcgt ggtctcactc tctcttctgc 300
atctctactc ttaagagact caggccaaga aacgtcttct aaatttcccc atcttctaaa 360
cccaatccaa atggcgtctg gaagtccaat gtggcaagga aaaacagggtc ttcacgaat 420
ctactaattc cacacctttt attgacacag aaaaatgttg gaatcccaaa tttgattgat 480
ttgaagaaca tgtgagagggt ttgactagat gatggatgcc aatattaaat ctgctggagt 540
ttcatgtaca agatgaagga gaggcaacat cacttgaaa ataagaatag aaataaagga 600
tgtgggttga gaaatatgga cacttaatac taccttgaaa ataagaatag aaataaagga 660
tggtgatttg gaatggagat tcagttttca tttggttcat taattctata aggccataaa 720
acaggtaata taaaaagctt ccattgattct atttatatgt acatgagaag gaactccag 780
gtgttactgt aattcctcaa cgtattgttt cgacagcact aatttaatgc cgataactc 840
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aatgcttttt attattatta ttttttagac agtctcactt tgcgcccgag gccggagtgc 1200
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cagccatcaa aatgcttttt atttctgcat atgttgaata ctttttaca tttaaaaaaa 1500
tgatctgttt tgaaggcaaa attgcaaatt tgaaattaa gaaggcaaaa atgtaaaagg 1560
gtcaaaacta taaatcaagt atttggaag ttgaagactg aagctaattt gcattaaatt 1620
cacaaacttt tatactcttt ctgtatatac atttttttct tttaaaaaac aactatggat 1680
cagaatagcc acatttagaa cactttttgt tatcagtcaa tattttttag tagttagaac 1740
ctggtcctaa gcctaaaagt gggcttgatt ctgcagtaaa tcttttaca ctgcctcgac 1800
acacataaac ctttttaaaa atagacactc cccgaagtct tttgttcgca tggtcacaca 1860
ctgatgctta gatgttccag taatctaata tggccacagt agtcttgat accaaagtcc 1920
tttttttcca tcttttagaa actacatggg aacaaacaga tcgaacagtt ttgaagctac 1980
tgtgtgtgtg aatgaacact cttgctttat tccagaatgc tgtacatcta ttttgatttg 2040
tatatttgtt ttgtgtattt acgctttgat tcatagtaac ttcttatgga attgatttgc 2100
attgaacaca aactgtaaat aaaaagaaat ggctgaaaga gcaaaaaaaa aggaaagaaa 2160
aaagaaaaaa aaaagaaaaa aaaaaggggg aggc

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2194

(2) INFORMATION ON SEQ ID NO. 107:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1812 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```

cggaagggtg accttggtg aattttgacg agaacaagtt cgtggaccga agaagatggg 60
ggccgcacgc ccaggcccg gccccgacga ggccgaggtg gacacctgcc ccctgcgcaa 120
aggaacatg aaacagaccc tacaggcagc tctgaagaac cccctatca acaccaagag 180
tcaggcagtg aaggaccggg caggcagcat tgtcttgaag gtgctcatct cttttaaaagc 240
taatgatata gaaaaggcag ttcaatctct ggacaagaat ggtgtggatc tcctaataaa 300
gtatatttat aaaggatttg agagcccgtc tgacaatagc agtgctatgt tactgcaatg 360
gcatgaaaag gcacttgctg ctggaggagt agggctccatt gttcgtgtct tgactgcaag 420
aaaaactgtg tagtctggca ggaagtggat tatctgcctc gggagtggga attgctggta 480
caaagaccaa aacaaccaa tgccaccgct gccctgtggg tagcatctgt ttctctcagc 540
tttgcttctg tgctttttca tatctgtaaa gaaaaaaatt acatatcagt tgccttttaa 600
tgaaaatttg gataatatag aagaaattgt gttaaaaatg aagtgtttca tcctttcaaa 660
accatttcag tgatgtttat accaatctgt atatagtata atttacattc aagtttaatt 720
gtgcaacttt taacccctgt tggctggttt tttgttctgt tttgttttgt attattttta 780
actaatactg agagatttgg tcagaatttg aggccagttt cctagctcat tgctagtcag 840
gaaatgatat ttataaaaaa tatgagagac tggcagctat taacattgca aaactggacc 900
atatttcctt tatttaataa gcaaaatatg tttttggaat aagtgggtggg tgaataccac 960
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gttcagagca agaagtcttg ctttatacaa atgtatccat aaaatatcag agcttgttgg 1140
gcatgaacat caaacttttg ttccactaat atggctctgt ttggaaaaaa ctgcaaatca 1200
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aaccaaatca gttctcaaaa aatgaccggt gcttataaaa agttataaat atcgagttag 1560
tctaaaacaa accacctgac caagagggaa gtgagcttgt gcttagtatt tacattggat 1620
gccagttttg taatcactga cttatgtgca aactggtgca gaaattctat aaactctttg 1680
ctgtttttga tacctgcttt ttgtttcatt ttgttttgtt ttgtaaaaat gataaaactt 1740
cagaaaataa aatgtcagtg ttgaataaaa taaaaaaaca aattgaagaa gaggatggag 1800
atttcgactt gg

```

1812

(2) INFORMATION ON SEQ ID NO. 108:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 890 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

```

aacgactcct ggtaccttgc tcccattact tcccgttttc tcgatctgct gctcgtctca 60
ggctcgtagt tcgcttcaa catgccggaa ccagcgaagt ccgctccccg gcccaagaag120
ggctcgaaga aagccgtgac taaggcgcag aagaaggacg gcaagaagcg caaggcagcc180
gcaaggagag ctactccgta tacgtgtaca aggtgctgaa gcagggtccac cccgacaccg240
gcatctcttc taaggccatg ggaatcatga actccttcgt caacgacatc ttcgaacgca300
tcgcggtgga ggcttccccg ctggcgcatc acaacaagcg ctcgaccatc acctccaggg360
agatccagac ggccgtgctg ctgctgctgc ccggggagtt ggccaagcac gccgtgtccg420
agggcaccaa ggccgtcacc aagtacacca gcgctaagta aacttgccaa ggagggactt480
tctctggaat ttcctgatat gaccaagaaa gcttcttctc aaaagaagca caattgcctt540
cggttacctc attatctact gcagaaaaga agacgagaat gcaaccatac ctgatggac600
ttttccacaa gctaaagctg gcctcttgat ctcatcaga ttccaaagag aatcatttac660
aagttaattt ctgtctcctt ggtccattcc ttctctctaa taatcattta ctgttcttca720
aagaattgtc tacattaccc atctctctct ttgcctctga gaaagagtat ataagcttct780
gtaccccact ggggggttgg ggtaatatc tgtggtcctc agccctgtac cttaataaat840
ttgtatgcct tttctcttaa aaaaaaaaaa aagaagaagg aagaggatgc 890

```

(2) INFORMATION ON SEQ ID NO. 110:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2627 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```

ggcacgagat gtgaaaaggt tttgtgtaca ccacctccaa aaataaaaaa tggaaaacac 60
accttttagt aagtagaagt atttgagtat cttgatgcag taacttatag ttgtgatcct 120
gcacctggac cagatccatt ttcacttatt ggagagagca cgatttattg tggtgacaat 180
tcagtgtgga gtcgtgctgc tccagagtgt aaagtgggca aatgtcgatt tccagtagtc 240
gaaaatggaa aacagatata aggatttgga aaaaaatttt actacaaagc aacagttagt 300
tttgaatgag ataagggttt ttacctcgat ggcagcgaca caattgtctg tgacagtaac 360
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cactgcattt catatcacac tgttaaaagt tgtgttttga aattttatgt ttagtgtcac 1980
aaattggggc aaagaaacat tgccttgagg aagatatgat tggaaaatca agagtgtaga 2040
agaataaata ctgttttact gtccaaagac atgtttatag tgctctgtaa atgttccctt 2100
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gcaattacta agaagcagat aatgggtgtt tttagaaacc taattgaagt atattcaacc 2280
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tgacagaagc gtatatgaat tcaagaaaaa ttaagctgca aaaaatgtatt tgctataaaa 2520
tgagaagtct cactgataga ggttctttat tgctcatttt ttaaaaaatg gactcttgaa 2580
atctgttaaa ataaaattgt acatttgga aaaaaaaaaa gccaaaaa 2627

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(2) INFORMATION ON SEQ ID NO. 111:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 976 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

ctcgagccgc gagattcccc cgaagttctc catgaagcgc ctcaccgcgc gcctcatcgc 60
cgtcatcgtg gtggtcgtgg tggccctcgt cgccggcatg gccgtcctgg tgatcaccaal20
ccggagaaag tcggggaagt acaagaaggt ggagatcaag gaactggggg agttgagaaal80
ggaaccgagc ttgtaggtac ccggcggggc aggggatggg gtggggtagc ggatttcggt240
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gcctcagggg ctcctttctt tctcacttct gtcttgaagg aagcatttct aaaatgtatc420
ccctttcggg ccaacaacag gaaacctgac tggggcagtg aaggaaggga tggcatagcg480
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gcttgtcact gggaaagaag cctgtttcag ctgcctgaac gcagtttgga tgtctttgag780
gacagacatt gcccggaaac tcagtctatt tattcttcag cttgccetta ctgccactga840
tattggtaat gttctttttt gtaaaatgtt tgtacatatg ttgtctttga taatgttgct900
gtaatttttt aaaataaaac acgaatttaa taaaatatgg gaaaggcaca caaaaaaaaa960
aaaaaaaaaa aaaaac

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976

(2) INFORMATION ON SEQ ID NO. 112:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1427 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```

cttcgggggt gactgcctct tccagggcgg gcggtgtggt gcacgcattg ctgtgctcca 60
actccctcag ggctgtgttt gccgcactct gctgctatga gcttcctcaa aagtttcccg 120
ccgcctgggc cagcggaggg gctcctgcgg cagcagccag acactgaggc tgtgctgaac 180
gggaaggggc tcggcactgg taccctttac atcgctgaga gccgcctgtc ttggttagat 240
ggctctggat taggattctc actggaatac cccaccatta gtttacatgc attatccagg 300
gaccgaagtg actgtctagg agagcatttg tatgttatgg tgaatgccaa atttgaagaa 360
gaatcaaaaag aacctgttgc tgatgaagaa gaggaagaca gtgatgatga tgttgaacct 420
attactgaat ttagatttgt gcctagtgtat aaatcagcgt tggaggcaat gttcactgca 480
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gaaggaatgc tttctcagtc tgtgagcagc cagtataata tggctggggg caggacagaa 720
gattcaataa gagattatga agatgggatg gaggtggata ccacaccaac agttgctgga 780
cagtttgagg atgcagatgt tgatcactga aaatgattta tgcaagttta agattctgct 840
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tggttaattgt tttgtttttg taatagctta acaataaac ctaggttttc tatattaaaa 1380
aaaaaaaaaa aaaaaaaaaa aaggtacctg ccctaataat attctgc 1427

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(2) INFORMATION ON SEQ ID NO. 113:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2639 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

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tccctatctt acccttcccg attctccttt tttcttttct ttttttatat ggctttcttc 60
ttttctttct ttcttttttc ttcccttttt tatttgacca gtgtaaataa caaacattta 120
ttggtgtcac ttatggtaga aaaaacttcc tacaccagat gcacatgacc cagttgttaa 180
atagaacatt ttgaagggtga acacacaccc taacccaggt tttttaccog ctttttaaga 240
tggccaattc ttcttctccc ccccacccaa agacatgtga gcaactgcta atgaaaagca 300
gtaaacagcc gcttaggcta tagcagtttc aactccactc tgagggtgaag attccaatta 360
cattcgagac ttaagtctct tcaatttttt cctaacaaaa gtctctgagt ccagtattta 420
caatattaca gcactagcag atcagtgtct acaactcatc tttttctgct gtatcctctt 480
caccagttgg gggaggggcct gcacttccat agagtttgct gataattggg tgaacaattt 540
cttccagttc cttcttctta gctttgaagt cttcaatgtc agcatcttgg tggctttcca 600
gccattcaat cttttctttt acagcttttt ccattggtct cttatcttca gaggaaagt 660
tacctcccag cttttcttta tctccaatct gattctttag agaataggca tagctttcca 720
actcatttct agtatcaatg cgctccttga gctttttgtc ttcttcagca aacttctcag 780
catcattaac catcctttct atttcttcag gtgtcaggcg attctgggtc ttggtgattg 840
tgatcttatt ttgttccct gtacccttgt cttcagctgt cactcgaaga ataccattca 900
catctatctc aaagggtgact tcaatctgtg ggacccacag aggagcagga ggaattccag 960
tcagatcaaa tgtaccaga agatgattgt cttttgtcag gggcttttca cttcatagaa 1020
ccttgattgt aacagtttgt tgattatcag aagctgtaga aaagatctga gacttcttgg 1080
taggcaccac tgtgttctct ggaatcagtt tggctatgac acctcccaca gtttcaatac 1140
caagtgtaa gggacatata tcaagcagta ccaggtcacc tgtatcttga tcaccagaga 1200
gcacaccagc ctggacagca gcaccatacg ctacagcttc atctgggttt atgccacggg 1260
atggttcctt gccattgaag aactctttaa ccagttgctg aatctttgga attcgagtcg 1320
agccaccaac aagaacaatt tcatcaatat cagacttctt caaatcagaa tcttccaaca 1380
cttctgggac gggcttcata gttagaccga acagatccat gttgagctct tcaaatttgg 1440
cccgagtcag ggtctcagaa aagtcttctc cttcatagaa ggactcaatt tcaattcttg 1500
cttgatgctg agaagacagg gcccgtttgg ctttttctac ctgcgcggcg agtttctgca 1560
cagctctatt gtcttctctg acatctttgc ccgtcttctt tttgtacagt ttgatgaagt 1620
gttccatgac acgctgggtc aagtcttctc caccagatg agtatctcca ttagtggcca 1680
caacttcgaa gacaccattg tcaatggtag gaagagacac atcgaaggtt ccgccaccca 1740
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ctgcggtagg ctggttgatg atctcataa catttaggcc agcaatagtt ccagcgtctt 1860
tgggttgctt gcggtgggca tcattaaaat aggtctgtac agtaacaact gcatgggtaa 1920
ccttctttcc caaataagcc tcagcgggtt ctttcatttt agtgagaacc atggaagaa 1980
ttcttccagg agcaaatgtc ttgttttgcc cacctccaat atcaacttga atgtatggt 2040
tagttttctt ttcaaccacc ttgaacggca agaacttgat gtctgtctgc acagacgggt 2100
cattccacgt gcggccgatg agccgcttgg cgtcaaagac cgtgttctcg ggttggagg 2160
tgagctgggt cttggcggca tcgccaatca gacgttcccc ttcaggagtg aaggcgacat 2220
aggacggcgt gatgcggttg cctgatcgt tggcgatgat ctccacgcgg ccgttcttga 2280
acacgcccag gcaggagtat gtggtccccg ggtcgatgcc gaccaccgtg ccacgtctct 2340
ccttcttgtc ctctcctcgt gccgcgcgcg cgctgagcag cagcagcatc gcggccacca 2400
gggagagctt catcttgcca gccagttggg cagcagcagg cagtcagacc acagggcgta 2460
gcacaggagc acagcgcaat ttccgacttg caggcgagc gggcccgagg tcacaaggcg 2520
ccacgaacca ggcgaagggc aggtctagaa atacaggccg cggcgcttcc ctctcacact 2580
cgcgaaacac cccaataggt caatctgtct gtgctgtctt ggccggcatc gacccttag 2639

```

(2) INFORMATION ON SEQ ID NO. 114:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 634 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```
ctccccgcgcg cgcggttaaa tccccgcacc tgagcatcgg ctcacacctg caccgccgcc 60
gggcataagca ccatgcctgc ttgtcgcccta ggcccgctag ccgcccgcct cctcctcagc120
ctgctgctgt tcggcttcac cctagtctca ggcacaggag cagagaagac tggcgtgtgc180
cccgagctcc aggtgacca gaactgcacg caagagtgcg tctcggacag cgaatgcgcc240
gacaacctca agtgctgcag cgcgggctgt gccaccttct gctctctgcc caatgataag300
gagggttctt gccccaggt gaacattaac ttccccagc tcggcctctg tcgggaccag360
tgccaggtgg acagccagtg tcttgccag atgaaatgct gccgcaatgg ctgtgggaag420
gtgtcctgtg tcaactccaa ttcttgagct ccagccacca ccaggctgag cagtgaggag480
agaaagtttc tgcttgccc tgcattctgt tccagcccac ctgccctccc ctttttcggg540
actctgtatt cctcttggg ctgaccacag cttctccctt tcccaaccaa taaagtaacc600
actttcagca aaaaaaaaaa aaaaaaaca aaaa 634
```

(2) INFORMATION ON SEQ ID NO. 115:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 719 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN

(vii) OTHER ORIGIN:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

gtcgactttt	tttttttttt	tttaacatgg	aaaagtattt	ttaaaaaatcg	aataatccta	60
ttcaagtc aa	ccagtggtaa	ccccgggtgtg	cttcctgcc a	gtctgttctc	ccccatggga	120
gtcacacaaa	atgaaaatct	cctagaaaaga	gaagacaaa g	accgcgaaaa	gatgtatgcc	180
accatctatg	agctgaaaga	agacaaagag	tacaatgtca	cctccgtcct	gtttaggaaa	240
aagaagtggtg	actactggat	caggactttt	gttcagggtt	gccagcccg	cgagtttcacg	300
ctgggcaaca	ttaagaggtta	ccctggatt a	acgagttacc	tcgtccgag	ggtgtgaccc	360
aactacaacc	agcatgctat	gggtgttcttc	aagaaaagtt	ctcaaaacag	ggagtaacct	420
aagatcacc	tctacgggag	aaccaaggag	ctgacttcgg	aactaaagga	gaacttcatc	480
cgtcttctcca	aatctctggg	cctccctgaa	aaccacatcg	tcttccctgt	cccaatcgac	540
cagtgctatcg	acggctcgat	gcacaggtgc	cgccagctgc	cgcaccagcc	cgaaccaccc	600
tgaggggagct	gggagaccct	ccccacagt g	ccacccatgc	agctgtctcc	caggccacccc	660
cgctgatgga	gccccacctt	gtctgctaaa	taaacatgtg	ccctcaaaaa	aaaaaaaaaa	71

(i) SEQUENCE CHARACTERISTIC:

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

gtcgataacg ccagacgcaa gacgccgggc ctacagcggg agcgtgagga aagccgtgcg 60
ttgcgttcca aggcattctg gagcccgcg agtatacacc atgagcaaag ctcaccctcc120
cgagttgaaa aaatttatgg acaagaagtt atcattgaaa ttaaattggt gcagacatgt180
ccaaggaata ttgcggggat ttgatccctt tatgaacctt gtgatagatg aatgtgtgga240
gatggcgact agtggacaac agaacaatat tggaaatggt gtaatacgag gaaatagtat300
catcatgtta gaagccttgg aacgagtata aataatggct gttcagcaga gaaacccatg360
tcctctctcc atagggcctg ttttactatg atgtaaaaat taggtcatgt acattttcat420
attagacttt ttgttaaata aacttttgta atagtcaaaa aaaagtttgg tctcatctac480
cttataatat ctgc

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494

(2) INFORMATION ON SEQ ID NO. 117:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```

acggggctga ctacgctcaa agctccattg ttagatecct tctgtcctcc ttctgggctc 60
ctccttcctc ccacccctc taataggctc ataagtgggc tcaggcctct ctgcggggct 120
cactctgcgc ttcacatggg ctttcattgc caagtccctc tatgacctca gtgccatcag 180
cctggatggg gagaaggtag atttcaatac gttccggggc agggccgtgc tgattgagaa 240
tgtggcttcg ctctgaggca caaccacccg ggacttcacc cagctcaacg agctgcaatg 300
ccgctttccc aggcgcctgg tggtccttgg cttcccttgc aaccaatttg gacatcagga 360
gaactgtcag aatgaggaga tcctgaacag tctcaagtat gtccgtcctg ggggtggata 420
ccagcccacc ttcacccttg tccaaaaatg tgagggtgaat gggcagaacg agcatcctgt 480
cttcgcctac ctgaaggaca agctccctta cccttatgat gacctttt ccctcatgac 540
cgatcccaaag ctcatcattt ggagccctgt gcgccgctca gatgtggcct ggaactttga 600
gaagtccctc atagggccgg agggagagcc cttccgacgc tacagccgca ccttcccaac 660
catcaacatt gagcctgaca tcaagcgcc ccttaaagtt gccatataga tgtgaactgc 720
tcaacacaca gatctctac tccatccagt cctgaggagc cttaggatgc agcatgcctt 780
caggagacac tgctggacct cagcattccc ttgatatacag tccccttcac tgcagagcct 840
tgcccttccc ctctgcctgt ttccctttcc tctcccaacc ctctggttgg tgattcaact 900
tgggctccaa gacttgggta agctctgggc cttcacagaa tgatggcacc ttcctaaacc 960
ctcatgggtg gtgtctgaga ggcgtgaagg gcttgagacc actctgctag aagagaccaal1020
taaaaggcag gtgtggaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa

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1065

(2) INFORMATION ON SEQ ID NO. 120:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 648 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```

ggactgccgt cgtaggtctc cggcgagttg ttgcctgggc tggacgtggt tttgtctgct 60
ggcccccgtc ttgcggtctt cgtttcattt tctgcagcgc gccagcagga tggcccacaal20
gcagatctac tactcggaca agtacttcga cgaacactac gagtaccggc atgttatgtt180
acccagagaa ctttccaaac aagtacctaa aactcatctg atgtctgaag aggagtggag240
gagacttggt gtccaacaga gtctaggctg ggttcattac atgattcatg agccagaacc300
acatatctct ctcttttagac gacctcttcc aaaagatcaa caaaaatgaa gtttatctgg360
ggatcgtaa atctttttca aatttaattgt atatgtgtat ataaggtagt attcagtga420
tacttgagaa atgtacaaat ctttcatcca tacctgtgca tgagctgtat tcttcacagc480
aacagagctc agttaaatgc aactgcaagt aggttactgt aagatgttta agataaaagt540
tcttccagtc agtttttctc ttaagtgcct gtttgagttt actgaaacag tttacttttg600
ttcaataaaag tttgtatggt gcatttcaaaa aaaaaaaaaa aaagtcga 648

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(2) INFORMATION ON SEQ ID NO. 121:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1842 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

```

ctcgagccgc tcgagccgct gctctctgga gggggtagag atcaaaggcg gtccttccg 60
acttctccaa gagggccagg cactggagta cgtgtgtcct tctggcttct acccgtaacc 120
tgtgcagaca cgtacctgca gatctacggg gtcctggagc accctgaaga ctcaagacca 180
aaagactgtc aggaaggcag agtgcagagc aatccactgt ccaagaccac acgacttcga 240
gaacggggaa tactggcccc ggtctcccta ctacaatgtg agtcatgaga tctctttcca 300
ctgctatgac ggttacactc tccggggctc tgccaatcgc acctgccaag tgaatggccg 360
gtggagtggg cagacagcga tctgtgacaa cggagcgggg tactgctcca acccgggcat 420
ccccattggc acaaggaagg tgggcagcca gtaccgcctt gaagacagcg tcacctacca 480
ctgcagccgg gggcttacct tgcgtggctc ccagcggcga acgtgtcagg aagggtggctc 540
ttggagcggg acggagcctt cctgccaaga ctccctcatg tacgacaccc ctcaagaggt 600

ggccgaagct ttctgtctt ccctgacaga gaccatagaa ggagtcgatg ctgagggatgg 660
gcacggccca ggggaacaa agaagcggaa gatcgtcctg gacccttcag gctccatgaa 720
catctacctg gtgctagatg gatcagacag cattggggcc agcaacttca caggagccaa 780
aaagtgtcta gtcaacttaa ttgagaaggt ggcaagttat ggtgtgaagc caagatatgg 840
tctagtgaac tatgccacat accccaaaat ttgggtcaaa gtgtctgaag cagacagcag 900
taatgcagac tgggtcacga agcagctcaa tgaaatcaat tatgaagacc acaagttgaa 960
gtcagggact aacaccaaga aggccttcca ggcagtgtac agcatgatga gctggccaga 1020
tgacgtccct cctgaaggct ggaaccgcac ccgccatgtc atcatcctca tgactgatgg 1080
attgcacaac atgggcgggg acccaattac tgtcattgat gagatccggg acctgtctata 1140
cattggcaag gatcgcaaaa acccaaggga ggattatctg gatgtctatg tgtttgggggt 1200
cgggcctttg gtgaaccaag tgaacatcaa tgctttggct tccaagaaag acaatgagca 1260
acatgtgttc aaagtcaagg atatggaaaa cctggaagat gttttctacc aaatgatcga 1320
tgaaaagccag tctctgagtc tctgtggcat ggtttgggaa cacaggaagg gtaccgatta 1380
ccacaagcaa ccatggcagg ccaagatctc agtcattcgc ccttcaaagg gacacgagag 1440
ctgtatgggg gctgtgggtgt ctgagtactt tgtgttgaca gcagcacatt gtttcaactgt 1500
ggatgacaag gaacactcaa tcaaggtcag cgtaggaggg gagaagcggg acctggagat 1560
agaagtagtc ctatttcacc ccaactacaa cattaatggg aaaaaagaag caggaattcc 1620
tgaattttat gactatgacg ttgccctgat caagctcaag aataagctga aatatggcca 1680
gactatcagg cccatttgtc tcccctgcac cgaggggaaca actcgagctt tgaggcttcc 1740
tccaactacc acttgccagc aacaaaagga agagctgctc cccgcagaag agcaaagaaa 1800
getgtgtttg tccgggggga gaaaaaacc gccccggggg gg

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1842

(2) INFORMATION ON SEQ ID NO. 122:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1596 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```

ggcgggtata aaagccccac ccaggccagc cggtcttgct cagcatttgg ggacgctctc 60
agctctcggc gcacggccca gcttccttca aaatgtctac tggtcacgaa atcctgtgca 120
agctcagctt ggagggtgat cactctacac ccccaagtgc atatgggtct gtcaaagcct 180
atactaactt tgatgctgag cgggatgctt tgaacattga aacagccatc aagaccaaag 240
gtgtggatga ggtcaccatt gtcaacattt tgaccaaccg cagcaatgca cagagacagg 300
atattgcctt cgcctaccag agaaggacca aaaaggaact tgcacagca ctgaagtcag 360
ccttatctgg ccacctggag acggtgattt tgggcctatt gaagacacct gctcagtatg 420
acgcttctga gctaaaagct tccatgaagg ggctgggaac cgacgaggac tctctcattg 480
agatcatctg ctccagaacc aaccaggagc tgcaggaaat taacagagtc tacaaggaaa 540

tgtacaagac tgatctggag aaggacatta tttcggacac atctggtgac ttccgcaagc 600
tgatgggtgc cctggcaaaag ggtagaagag cagaggatgg ctctgtcatt gattatgaac 660
tgattgacca agatgctcgg gatctctatg acgctggagt gaagaggaaa ggaactgatg 720
ttcccaagtg gatcagcatc atgaccgagc ggaggggccc cacctccaga aagtatttga 780
taggtacaag agttacagcc cttatgacat gttggaaaagc atcaggaaaag aggttaaagg 840
agacctgcaa aatgctttcc tgaacctggg tcaagtgcatt cagaacaagc cctgtatatt 900
tgctgatcgg ctgtatgact ccatgaaggg caaggggacg cgagataagg tcttgatcag 960
aatcatggtc tcccgccagt aagtggacat gttgaaaatt aggtctgaat tcaagagaaa 1020
gtacggcaag tccctgtact attatatcca gcaagacact aagggcgact accagaaagc 1080
gctgctgtac ctgtgtgggt gagatgactg aagcccgaca cggcctgagc gtccagaaaat 1140
gggtgctcacc atgcttccag ctaacagggtc tagaaaacca gcttgcaaat aacagtcccc 1200
gtggccatcc ctgtgagggt gacgttagca ttacccccc aa cctcatttta gttgcctaag 1260
cattgcctgg ccttctgtgc tagtctctcc tghtaagcaa agaaatgaac attccaagga 1320
gttggaaagt aagtctatga tgtgaaacac tttgcctcct gtgtactgtg tcataaacag 1380
atgaataaac tgaatttgta ctttagaaac acgtactttg tggccctgct ttcaactgaa 1440
ttgtttgaaa attaaacgtg cttgggggttc agctggtgag gctgtccctg taggaagaaa 1500
gctctgggac tgagctgtac agtatggttg cccctatcca agtgtcgcta tttaaagtaa 1560
atataaatga aataaaataa aataaaatca aaaaaa
1596

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(2) INFORMATION ON SEQ ID NO. 123:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

gtcgcagctg accctcgctc ccgccccccg ctggagtcg acgtggaagt tgctggctga 60
ctgggcttgc gaggaaccg cctcgagct gcagccgaag gcaaggaatc actgaagatc 120
ggcgagggag gacagggggg tcatcatggg tggcttttcc tcaagtatat tttccagtct 180
gtttggaact cgggaaatga gaattttaat tttgggatta gatggagcag gaaaaaccac 240
aattttgtac agattacaag tgggagaagt tgttactact atacctacca ttggatttaa 300
tgtagagacg gtgacgtaca aaaaccttaa attccaagtc tgggatttag gaggacagac 360
aagtatcagg ccatactgga gatgttacta ttcaaacaca gatgcagtca tttatgtagt 420
agacagtgtg gaccgagacc gaattggcat ttccaaatca gagttagttg ccattgttga 480
ggaagaagag ctgagaaaaa ccatttttagt ggtgtttgca aataaacagg acatggaaca 540
ggccatgact tcctcagaga tggcaaattc acttgggtta cctgccttga aggaccgaaa 600
atggcagata ttcaaaacgt cagcaaccaa aggcaccggc cttgatgagg caatggaatg 660
gttagttgaa acattaaaaa gcagacagta attcagtcca ttcttctccc ctgaaatgaa 720
gactacatca cctctctccc tttggaaaca gtcaagtgtt cttcacacta ctagatgtta 780

aaactatatg attattggca tatactgact gactgcaata tttgtagtaa atagggaaaa 840
taagtattta gttggaggga taatttgatc gaatcacctg aatgttctat gtaatgtaaa 900
atattctttt cttgctttct tgtgttaagg tatatatctt atttgtatgg aattcttatt 960
caaatacagt tctattaaag agtatactcc tattggatga aaaaaacctt aaaaaaaaaa 1020
aaaaaaaaaa aaa                                     1033

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(2) INFORMATION ON SEQ ID NO. 124:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 65 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

ICLLVHFVSR AKTVNLTF SY WWVITENKDL FSCSLKSHK NNQIGSCLLS CVSWFLTCVH60
TPVCL 65

(2) INFORMATION ON SEQ ID NO. 125:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 64 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

ISVFRLEFKYL THFQTCTMEFY KPLDFQQHTI ENTCYSKHNF SVSSIAVVRD NIAISGMLQA60
FKIA 64

(2) INFORMATION ON SEQ ID NO. 126:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 61 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

KANLLPATPE GTQIWVGPFV QLGKRMGKPG DGFHKFSSGL WHSFQEIPLG KGLLANMHFQ60
T 61

(2) INFORMATION ON SEQ ID NO. 127:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

LKNTNEVKAL NWYTLFTPIF QVWKCIFASR PLPRGISWKE CHNPLENLWK PSPGFPIRLP60
 SWKTGPTHIW VPSGVAGRRF AF 82

(2) INFORMATION ON SEQ ID NO. 128:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

HTWDPYPLGI SPRTIRPVCQ PKVAFGMLNF PLSKKVHLPN EVTIRLNPKK SLDFVFYKNS60
 TFPIKSLVIK ISTLPKCDST AWFLANKNPI 90

(2) INFORMATION ON SEQ ID NO. 129:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

82

(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

70

(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

AIQCEAYFIA TLVDCQGDSA TVLDKLMFPF SLAANRRATY SAGSRARSWG SRGYTSSLI I60

(i) SEQUENCE CHARACTERISTIC:


```

LSEDEIRTLK QKKIDETSEQ EOKHKETNNS NAQNPSEEEG EGQDEDILPL TLEEKENKEY 60
LKSLFEILIL MGKQNIPLDG HEADEIPEGL FTPDNFQALL ECRINSGEV LKRKFETTAV120
NTLFCCKTQQ RQMLEICESC IREETLREVR DSHFFSIITD DVVDIAGEEH LPVLVRFVDE180
SHNLREEFIG FLPYEADAEI LAVKFHTMIT EKWGLNMEYC RGQAYIVSSG FSSKMKVVAS240
RLEKYPQAI YTLCCSCALN MWLAKSVPM GVSVALGTIE EVCSFFHRSP QLLLELDNVI300
AVLFQNSKER GKELKEIHS QWTGRHDAFE ILVELLQALV LCLDGINS DT NIRWNNYIAG360
RAFVLCSAVS DFDFIVTIVV LKNVLSFTRA FGKNLQGQTS DVFFAAGSLT AVLHSLNEVS420
GKY

```

(2) INFORMATION ON SEQ ID NO. 134:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 237 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

VENIEVYHEF WFEEATNLAT KLDIQMKLPG KFERRAHQGNL ESQLTSESYY KETLSVPTVE 60
 HIIQELKDIF SEQHLKALKC LSLVPSVMGQ LKENTSEHH ADMYRSDLPN PDTLSAELHC120
 WRIKWKHRGK DIELPSTIYE ALHLPDIKFF PNVYALLKVL CILPVMKVEN ERYENGRKRL180
 KAYLRNTLTD QRSSNLALLN INFEDIKHLD LMVDYIKLY TSKSELPTDN SETVENT 237

(2) INFORMATION ON SEQ ID NO. 135:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 89 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

RIRINGSLCP QTKNNLYFHI VELSIGASV GERWYGMGES ILPARGESQG LLCLFYFYKEI60
 LPLFLVNKLR GTDVGLEQGL SGGEGSWTA 89

(2) INFORMATION ON SEQ ID NO. 136:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 82 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(vi) ORIGIN
(A) ORGANISM: HUMAN

EEERAKREEL ERILEENNRRK IAEAQAKLAE EQLRIVEEQR KIHEERMKLE QERQRQQKEE60
OKIILGKGKS RPKLSFSLKT QD 82

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 71 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(vi) ORIGIN
(A) ORGANISM: HUMAN

SALKVEYLLS CPVSCRVCSS AAIRASFLFK MICTVSLAIP ASAAQPFIKK QHTRKAELRN60
ADVYGKKEQK M 71

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 67 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(vi) ORIGIN
(A) ORGANISM: HUMAN

SSAQRKYFNL PVEILVMERC QTVLNGRTSK SEATVPTRRG LLYCSTFSAL YFLAEASPWS60
AMYKLGY 67

(2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

RAEKVEQYKS PRVVGTVASL LLVLPFKTVW HLSMTRISTG RLKYFLCAE

49

(2) INFORMATION ON SEQ ID NO. 140:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

SCERRGFIMA DDLKRFLYKK LPSVEGLHAI VVSDRDGVPV IKVANDNAPE HALRPGFLST 60
 FALATDQGSK LGLSKNKSII CYYNTYQVVQ FNRLPLVVSF IASSSANTGL IVSLEKELAP120

LFEELRQVVE VS

132

(2) INFORMATION ON SEQ ID NO. 141:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

QMIILFLESP SLLPWSVARA KVDKKPGRKA CSGALSFATL ITGTPSLSDT TMAWSPSTLG 60
NFLYKNRFRS SAMMNPLLSQ DQSPRLGFLG CLVLSAVTSG TALKTGSSSS HRHMIHDLVC120
APGSTF 126

(2) INFORMATION ON SEQ ID NO. 142:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 152 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

SAVKRGWDLN MAAVVAATAL KGRGARNARV LRGILAGATA NKASHNRTRA LQSHSSPEGK 60
EEPEPLSP EL EYIPRKRGN PMKAVGLAWA IGFP CGILLF ILTKREVDKD RVKQMKARQN120
MRLSNTGEYE SQRFRASSQS APSPDVGSGV QT 152

(2) INFORMATION ON SEQ ID NO. 143:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 114 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

EGRSAPQVCT PDPTSGDGAL WEEALNLWLS YSPVLDNRMF CRAFTCFTRS LSTSRIVRMK 60
RRIPQ GKPM A QASPTAFMGF LPLFLGMYSS SGRGSGSSL PSGELWLCRA RVLL 114

(2) INFORMATION ON SEQ ID NO. 144:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 267 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

EDEVEEESTA LQKTDKKEIL KKSEKDTNSK VKPKGKVRWT GSRTGRWKY SSNDESESG 60
 SEKSSAASEE EEEKESEAI LADDDPECKK CGLPNHPELI LLCDSGSGY HTACLRPPLM120
 IIPDGEWFCP PCQHKLLCEK LEEQLQDLV ALKKKERAER RKERLVYVGI SIENIIPPQE180
 PDFSEDQEEK KKDSKKSKAN LLERRSTRTR KCISYRDEF DEAIDEAIED DIKEADGGGV240
 GRGKDSTIT GHRGKDISTI LDEKIIT 267

(2) INFORMATION ON SEQ ID NO. 145:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 185 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

SSEKSGSCGG MMFSILIPTY TKRSFLRSAR SFFFKATSKS CNCSSNFSQS SLCWQGGQNH 60
 SPSPGMIIRGG RRQAVWYPLS QESHRRISG WFGPHFLHG SSSSARMASS LSFSSSSSEA120
 ADDFSLPDPS LSSLLEYFHL PRVREPVHRT LPLGFTLEFV SFSDFFKISF LSVFCKAVDS180
 SSTSS 185

(2) INFORMATION ON SEQ ID NO. 148:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 134 amino acids
- (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

KRQPTSAMKD PSRSSTSPSI INEDVIINGH SHEDDNPFAE YMWMENEEEF NRQIEEELWE 60
EEFIERCFQE MLEEEEEHEW FIPARDLPQT MDQIQDQFND LVISDGSSLE DLVVKSNLNP120
NAKEFVPGVK YGNI 134

(2) INFORMATION ON SEQ ID NO. 149:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 135 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

HSDKRAFTIK SSNTAFTVWK LCYIHQKRAP STQIFPYFTP GTNSFAFGFR LLLTTRSSRE 60
EPLITRSLN WSWIWSIVCG RSRAGINHSC SSSSSSISWK QRSINSSSHN SSSICLLNSS120
SFSIHMYSAN GLSSS 135

(2) INFORMATION ON SEQ ID NO. 150:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 58 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

LVSGANQCGS CNSKSFLTGA WYYRVGFRFF RGGLDFDFDF FFYVIFGKTH SELYLVT 58

(2) INFORMATION ON SEQ ID NO. 151:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

FFVLKSLLVG ACYWEQVFVQ KLOSESLCIT ETLFITSLLS LPQKTVGLNK IICILYLYKC60
L 61

(2) INFORMATION ON SEQ ID NO. 152:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

SACKFLRLDP LLTVDQLMYT CIKALNKSL WLITAKMGTR HLLCVLVTAV ALRAVRPCL160

(2) INFORMATION ON SEQ ID NO. 153:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids

(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

KRDIILNVFS QRS HKRKKNQ NQIN HHEKNE TPHGNTKLWL GSSYYYSSHI GWRRKP 56

(2) INFORMATION ON SEQ ID NO. 155:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 150 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```
IPVHRLHGRA DPLGWSIVSD LITSGLGAGV LRGLPARRLH SLGRRVLGRP GVWLERLGHG 60
RRDALGAWSA AQRPRTPGRP ACVCAPRRGP ESPSADPVPP PGRAGDPSPD DASASGPRGG120
AATKAGPAHD PGQLRPELRV LPPPPRGDRE                                     150
```

(2) INFORMATION ON SEQ ID NO. 156:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 81 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

LPVAAGGRGQ DAQLRPELSG VVSRPRLGGG APSRSRGRRI GVARVSSPAG RRDRVCGGGL60
GASAGRAHAG GAARGAGPLR G 81

(2) INFORMATION ON SEQ ID NO. 157:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 214 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

PGSQSVTPPM AEPLQPDPGA AEDAAAQAVE TPGWKAPEDA GPQPGSYEIR HYGPAKWVST 60
SVESMDWDSA IQTGFTKLNS YIQGKNEKEM KIKMTAPVTS YVEPGSGPFS ESTITISLYI120
PSEQQFDPPR PLESDVFIED RAEMTVFVRS FDGFSSAQKN QEQLLTLASI LREDGKVFDE180
KVVYTAGYNS PVKLLNRNNE VWLIQKNEPT KENE 214

(2) INFORMATION ON SEQ ID NO. 158:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 62 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

PNFYRGFIEN LTMCGGLSCL NLFRAVCSVH QMGRSGMGHL RPFRLSGLNRM LEPRLDSDL60
RF 62

(2) INFORMATION ON SEQ ID NO. 159:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 104 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

IHLPKKLISF YLRGEVQFSF GSSESKHLIC WVKTPFLAF YVLSHNNSIK QEGKQKTKKK 60
KGKKKNLHGL VSLTKHVGAV CLGGAGYRTC QCLGFSINLA RDIK 104

(2) INFORMATION ON SEQ ID NO. 160:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

SLLSIRKIKQ NTSPARLTCV YIIYIKQRATP TSQQLG EISA VHAVVCQFGE ITPWKNWKNL60
LAGKNSFICI KSVLQKNPCG 80

(2) INFORMATION ON SEQ ID NO. 163:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 75 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

20250324 15:30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

PSIDLEAEES QRLLKVVWF SFKLLFLES RIYGYNVCSL FVHKIKPFKK LKKKKKRGEK60
 KREKKGKGRK RRGE 75

(2) INFORMATION ON SEQ ID NO. 164:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 68 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

KYLTLPYKLL VPFCIPPSIT LTKGIFYCKE YFILIYTSHE FLPLVTIQML PSIIQIAQP60
 FYVHNSLL 68

(2) INFORMATION ON SEQ ID NO. 165:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 66 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

LFFLFRYHTV PLPPKGRVLI HWMTLCQTQM KLMAIPLVFQ IMFGILNGLY HYAVFEETLE60
 KTIHEE 66

(2) INFORMATION ON SEQ ID NO. 166:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 159 amino acids

```
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN
      (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:
```

(2) INFORMATION ON SEQ ID NO. 167:

(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

```
EPVAQKSQLD RTVCISDAGA CGETLSVTSE ENSLVKKKER SLSSGSNFCS EQKTSGIINK240
FCSAKDSEHN EKYEDTFLES EEIGTKVEVV ERKEHLHTDI LKRGSEMDNN CSPTRKDFTE300
DTIPRQTQHR RKTSLYFSSK YNKEALSPPR RKAFFKKWTPP RSPFNLVQET LFHDPWKKLLI360
ATIFLNTSG KMAIPVLWKF LEKYPsAEVA RTADWRDvSE LLKPLGLYDL RAKTIVKFSd420
EYLTQWKYP IELHGIGAP
```

(2) INFORMATION ON SEQ ID NO. 168:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

DCGKVQTQMQ FALTNFLGLI SLCKTPVLSF LPQDRVQSFL KHALRCPHLR HCFVDTLKGV60
 HKAKKSDQML RASNLYLTTW TWHWQKSLQH 90

(2) INFORMATION ON SEQ ID NO. 169:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

SDFCQCHVQV VRYKLLALSI WSDFFALWTP LRVSTKQCLR CGHLRACFRK LCTLSCGRKE60
 RTGVLHKEIS PRKLVNANCI CVCTLPQSYI VF 92

(2) INFORMATION ON SEQ ID NO. 170:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

ADSHQNYIPW PPACVLLARP WLASLTREKD LQKIRLWDHF VCALGMTFFP TPGKPLGLSE60
TLWLANHMLS LKVERLSNPP IPREFQSDV I 91

(2) INFORMATION ON SEQ ID NO. 171:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 95 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

NGGLNAHLAS ASEFDHSGVQ LIEREEECICI FYEKINIQEK MKLNGEIEIH LLEEKIQFLK60
MKIAEKQRQI CVTQKLLPAK RSLDADLAVL QIQFS 95

(2) INFORMATION ON SEQ ID NO. 172:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 90 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

KTEFGAQLGR HPGTSQLAVI SGSHKEVFAS QQSSFSGIGS FLPVDVFQFL HLVSSSLGYL60
FFHKKCIFLL PALSAERHYG QIQRQLSGH 90

(2) INFORMATION ON SEQ ID NO. 173:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

AVRSRGALSL SVGAACGLVA LWQRRRQDSG TMSGFSTEER AAPFSLEYRV FLKNEKGQYI 60
 SPFHDIPIYA DKVRHPCFWT QSLYSDQLVL HMNFICLST SA 102

(2) INFORMATION ON SEQ ID NO. 174:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

VKRLCPKTRM PYLICINWNI MKWRYILSFL IFEEDSVLQG EGRGALLGAE AAHSAGVLPP60
 PLPQSHQPAR GAD 73

(2) INFORMATION ON SEQ ID NO. 175:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

RRQRKAEPGA CALGRVGSEC IPEPGARRTA QAAGLRVSG AANTKVRELK HFRFLGLLRS 60
 CRSEMEVDAP GVDGRDGLRE RRGFSEGGRO NFDVRPQSGA NGLPKHSYWL DLWLFILFDV120
 VVFLFVYFLP 130

(2) INFORMATION ON SEQ ID NO. 176:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 62 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

ILKMATNFLN KEDRTLNRRI SHLQGTLPFI LHFVTNLQNS INWVGHPFL AKFLKLNPLV60
 RV 62

(2) INFORMATION ON SEQ ID NO. 177:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 174 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

AVYCILHQOK VLRLYKRALR HLESWCVORD KYRYFACLMR ARFEEHKNEK DMAKATQLLK 60
 EAESEFWYRQ HPQPYIFPDS PGGTSYERYD CYKVPWCOLD DWHPSEKAMY PDYFAKREQW120
 KKLRRRESWER EVKQLQEETP PGGPLTEALP PARKEGDLPP LWYIVTRPR ERPM 174

(2) INFORMATION ON SEQ ID NO. 178:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 131 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

PLVPSFPSAV SSTVLSWQSN QDTLPSQKDA SHLSTILGPC SNRISHRRCP QESQGRMAV 60
DADGTRILPR PPSAAGWPSP YPFHSYVLQT GLSSNKQSIG ICLSGRTTTR GGVA PAYKAA120
TPFADVVCNI R 131

(2) INFORMATION ON SEQ ID NO. 179:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

LMMTIYALSN EFAFKINEEQ LSFFPLLSVQ LWHAQRFLLD SWSGVIPFF FSCSCLPFLY60
PPKWRQIHDL KDTQYLLNSS 80

(2) INFORMATION ON SEQ ID NO. 180:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 140 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

KVLRKIKSPE EASQMAGAG PTMLLREENG CCSRRQSSSS AGDSGGERED SAAERARQQL 60
 EALLNKTMRI RMTDGRITLVG CFLCTDRDCN VILGSAQEFL KPSDSFSAGE PRVLGLAMVP120
 GHHIVSIEVQ RESLTGPPYL 140

(2) INFORMATION ON SEQ ID NO. 181:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

SLKGKRHRGQ RYGGPVRLSL CTSMETMWCP GTMARPSTRG SPAEKESDGL RNSCAEPRMT 60
 LQSRVQRKQ PTSVRPSVMR MRIVLSSAS SCCRARSAAE SSRSPSESPA LELL 114

(2) INFORMATION ON SEQ ID NO. 182:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

RLSRLTEPKE DPMAGISTAE HHLOPTAALP TQLSRSRHSP QVISTDGGGET RGCGRQERKA60
 ERRVCKNAKV TFPVVGKQ RHWFOCHRQS EHLEL 95

(2) INFORMATION ON SEQ ID NO. 183:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

RRVQHPPFFS QLIRDAAKRT FRITRLQAFS KYLVVYVYLN GSMLPVPSPC PLCQPPVALV 60
 LVSFPSSAKR PWNLNGGCFA LGGSCWWDQS FDKPPAPWWH LSWKDVTPG AQTACGSRTS120
 AFGIFLPQWG R 131

(2) INFORMATION ON SEQ ID NO. 184:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

TAPCCRC PAP VPSVNPLSLW CWFRSRLQQN DLGTSMGAAL LWEVLVGTR ALTNLLLLGG 60
 TSPGRTSQLQ VLRLPVAAEP VPLAFSSHNG EGDFGILTNS SLGLSLLPST ASRFSSICAY120
 YLRTVSAP 128

(2) INFORMATION ON SEQ ID NO. 185:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

DSRVYCFSGN YRKLVLPRKT GAIRNGSNIS KLRKQDVLSF AHLGFLLPF SLFSLRSLFQ60
FPSDLPLVPL ESQRL 75

(2) INFORMATION ON SEQ ID NO. 186:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 62 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

LGDSSEMPLL ALKCPVRLG TLEPSEILII LGSSPYFQMF SAQHWVLSST TENPEEKGR60
FP 62

(2) INFORMATION ON SEQ ID NO. 187:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 89 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

PHPSRRLTQG RWVRKSRVAM EKIPVSAFLR LVALSYNLAR DSTVKPGAKK DRKESRAKLR60
QTLRSWGEQ LIWTQTYEEA LYKSRLATN 89

(2) INFORMATION ON SEQ ID NO. 188:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

GNPELPWRKF QCQHSICALWR SPTIWPGIAQ SNLEPKRTGR SLEPNCARPS PEVGVNNSSG60
LRRMKKLYIN RD 72

(2) INFORMATION ON SEQ ID NO. 189:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

SLGHRPRNGG HSRGCDLGGL HAHSPDPRLO GAGLQAKNA AYSVSLPPGC VGHLPWHLRL 60
HHRTGREHRA HTLLPLWDPL FHLLLLPAGS CCQSDQARPG EEAPFPVGDS GSGRGLQSP120
GCYRY 125

(2) INFORMATION ON SEQ ID NO. 190:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 200 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

RGRDSCPRSP PALRSSPAAL LRAGSSTKFT ANALALGSRM ATTVPDGC RN GLKSKYYRLC 60
 DKAEAWGIVL ETVATAGVVT SVAFMLTLPI LVCKVQDSNR RKMLPTQFLF LLGVLGIFGL120
 TFAFIIGLDG STGPTRFFLF GILFSICFSC LLAHAVSLTK LVRGRKPLSR LVILGLAVGF180
 SLVQDVIAIE YIVLTMNRTK 200

(2) INFORMATION ON SEQ ID NO. 191:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 111 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

AEAHGQTQNH QPGKGLPPPD ELGQTDMSMQ QAGEADGKED PKEEEACGPC APVQSDDEGE 60
 GEAKDAQHTQ EEEKLSRQHF SPVGVLHLAD EDRESEHEGH RGHNPGCGHR F 111

(2) INFORMATION ON SEQ ID NO. 192:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 92 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

EIYWETDYNH SGTIDAHEMR TALRKAGFTL NSQVQQTIAL RYACSKLGIN FDSFVACMIR60
 LETLFKLFSL LDEDKDG MVQ LSLAEWLCCV LV 92

(2) INFORMATION ON SEQ ID NO. 193:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

ESLIAFLFLH DQCAQDSIVL TMIKDVVRIQ WTRNECKGGL EQRRGCPEGK ESYQILLNLQ60
PERLEFHRPQ SAPFHCSRHI K 81

(2) INFORMATION ON SEQ ID NO. 194:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

KTTIHGPCQN HLPPPHCFK RPTLSKGDQ IDSSQEGFRA SIRAWPVLP LLSEQQGFQG60
SGWHESLSLP SCSFMTNVPR TQ 82

(2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

RPPPSRSSL AGQTNTQHS SARES

25

(2) INFORMATION ON SEQ ID NO. 196:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 71 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

TMPSLSSRR LNSLKRVSR IIQATKLSKL MPSLLHAYRR AMVCCTWLLR VKPAFLRAVL60
ISWASMVPEW L 71

(2) INFORMATION ON SEQ ID NO. 197:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 86 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

IRRNTSRISV HTWRRTPPYD SPACFSCSIV SLESGFFSC VSVFFSFDLS NFSISAISGL60
SDMVAEEKQS EAHEYERQFL ASRRSG 86

(2) INFORMATION ON SEQ ID NO. 198:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 101 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

HPFSTFPTLP PQAGKFDATL LASQCILGGA RLLTIRLLAS PVQSFLWKAV DFSLASLSSS 60
VSTYRISR SQ PYRVCQTWLR RKSKARTST SDSSSRLAAV A 101

(2) INFORMATION ON SEQ ID NO. 199:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 100 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

TPFPSPQLYP LKQVNSTQHF SHLSAYLA AH ASLRFACLL L LFNRF FGRQW IFLRLCLLQ 60
FRLIEFLDLS HIGFVRHGCG GKAKRGARVR ATVPRVSPQW 100

(2) INFORMATION ON SEQ ID NO. 200:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 153 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

GLTDQYLELN ALQEELGPFG LVILGFPSNQ FGKQEPGENS EILPSLKYYR PGGGFVPNFQ 60
 LFEKGDVNGE KEQKFYTFLEK NSCPPTAELL GSPGRLEWEP MKIHDIRWNF EKFLVGPDI120
 PVMRWYHRTT VSNVKMDILS YMRRQAALSA RGK 153

(2) INFORMATION ON SEQ ID NO. 201:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 249 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

LMPPPYPYPL PIMQGPRRGS SGRKPHSQSF YPHPRFSFLL HKRQAWHNCV SEPLWTRDNC 60
 PSVCMATQPR ICLETQGWS ICVYGLAQHP HIFFSFLFQM SPKETQVLGP MVLLKPEHHS120
 WQHLPHAHHT THHQPPSSFL KDPPEPPSPS HSAPETSQDN CERDGRVPQV RGGVSMKEGP180
 EALVGGPPLS PSVVPALSAF RLRLPGRDIT PAPLEDMLSS HSVHWYLNTP ICPVKVFLQQ240
 KKKRKKKKK 249

(2) INFORMATION ON SEQ ID NO. 202:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 156 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

AGLSAPPPAP LLCRAQAPLA LGPNFSYRHG VRPGSSPGAH LPEARCGGGP RGRSQAQSPQ 60
 SSGPVGGGRGR SGSKARTPQL FRLQQQLQRF GHGCEVPRCW LQAAREHPGQ GQEAQSEEEG120
 EGQEGEGQEE GGSPLKGPQ GSLNLPCLR VPTTWS 156

(2) INFORMATION ON SEQ ID NO. 203:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 113 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

DPTSLTAMEF DLGAALPTS QKPGVGAGHG GDPKLSPHKV QGRSEAGAGP GPKQGHSSS 60
 DSSSSSSSDSD TDVKSHAAGS KQHESIPGKA KKPVKKKKEK GKKEKGKKKE APH 113

(2) INFORMATION ON SEQ ID NO. 204:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 162 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

GGPPPPKHLs SRWLVLVGRE EGLMSPVQGP SVGSLLLLLAL LLLALLLLH FGLLGLARDA 60
 LVLLGASSVG LHIRVRIAGA AAGVGRAVVS LLWTRTCPCL RPALNFVGTG LGISFVARPH120
 TGLLGGGLQG CSQVELHGGK RSWVLRPRAP GPCRGAEQGE ER 162

(2) INFORMATION ON SEQ ID NO. 205:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 145 amino acids
- (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

VEPWTTTCRAA GAVMADYWKS QPKKFCDYCK CWIADNRPSV EFHERGKNHK ENVAKRISEI 60
KQKSLDKAKE EEKASKEFAA MEAAALKAYQ EDLKRLGLES EILEPSITPV TSTIPPTSTS120
NQQKEKKEKK KKRSEFKQMG RRHNL 145

(2) INFORMATION ON SEQ ID NO. 206:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 262 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

PALSHLPRHQ INRKKRKRRR KKDPKGRWV EGITSEGYHY YYDLISGASQ WEKPEGFQGD 60
LKKTAVKTVW VEGLSGDGFT YYNTETGES RWEKPDDFIP HTSDLPSSKV NENSLGTLDE120
SKSSDSHSDS DGEQAEIEGG VSTETEKPKI KFKEKNKNSD GGSDPETQKE KSIQKQNSLG180
SNEEKSKTLK KSNPYGEWQE IKQEVESHEE VDLELPSTEN EYVSTSEADG GGEPKVVFE240

KTVTSLGVMA DGVAPVFKKR RT 262

(2) INFORMATION ON SEQ ID NO. 207:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 73 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

GKGRRKGIKG VCCNGGSCPE SIPRGFEKTW LRVRNFGAKH NTSNQHYPTY LDIKSTERKE60
REEEKKILQR ADG 73

(2) INFORMATION ON SEQ ID NO. 208:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 68 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

IWNFQALKMS MYQLQKLMVA ENPKWYLKKK QSLLELWQM EWPQSSKREE LENGKILGKF60
KGNEVMIQ 68

(2) INFORMATION ON SEQ ID NO. 210:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 194 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

SVHCFREDKM KFTIVFAGLL GVFLAPALAN YNINVNDNN NAGSGQQSVS VNNEHNVANV 60
DNNNGWDSWN SIWDYGNGFA ATRLFQKTC IVHKMNKEVM PSIQSLDALV KEKKLQGGKP120
GGPPPKGLMY SVNPNKVDDL SKFGKNIANM CRGIPTYMAE EMQEASLFFY SGTCYTTSVL180
WIVDISFCGD TVEN 194

(2) INFORMATION ON SEQ ID NO. 211:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

VHQALGRWSS WSLTLKLLFL DQCIKGLNGG HDFLVHVFVN ACLLLKESGC SKAISIIPDG60
 IPGVPSVVIV NIGHIVFIVD TH 82

(2) INFORMATION ON SEQ ID NO. 212:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

ELGLNHLWLR VWLEPTAQVP DVLFPFEMER EEKAVSLLLW FNVKEPQLPP LPGREAFGFL 60
 LLLLALVAGE VLQDHRLLAQ LVLAGLRAHA GRLRFRKALT KASARCAPEG WTSESFASF 119

(2) INFORMATION ON SEQ ID NO. 213:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

IICGCVSGLS PLHRSIMYCF QSSWRGRKRL YLCCSGLMSK SRSSLLCLAE KPLAFFFFSL 60
 RLWRVKYSRT TALRCSWSSR ACGLMRGVCA SGRPSRRPRP AVLLKAGHRS HSPLSETMHG120
 RSKSSFSDRF RRLMT 136

(2) INFORMATION ON SEQ ID NO. 214:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 101 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

TLETVHQGPV QWAQARHAAT DDSGQALKGR SSRGYYFSDK IQMPLLCGYR RNPSTGNKAH 60
FQNYHQRRPP ESYPAKLRV HCGNRWLYFL HLREQIPASV K 101

(2) INFORMATION ON SEQ ID NO. 215:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 204 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

LRCPAFRSTA GRGLREGLPE AQTPRMSPQA REDQLQRKAV VLEYFTRHKKR KEKKKKAKGF 60
 SARQRRELRL FDIKPEQQRY SLFLPLHELW KQYIRDLCSSG LKPDTPQPMI QAKLLKADLH120
 GAIISVTKSK CPSYVGITGI LLQETKHIFK IITKEDRLKV IPKLNCVFTV ETDGFISYIY180
 GSKFQLRSSE RSAKKFKAKG TIDL 204

(2) INFORMATION ON SEQ ID NO. 216:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 645 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

PTRPVAAGSE QQQQSAFIQE RQPVALMRLI SFNVPHIKNS TGEPIWKVLI YDRFGQDIIS 60
 PLLSVKELRD MGITLHLLH SDRDPIPDVP AVYFVMPTEE NIDRMCQDLR NQLYESYYLN120
 FISAISRSKL EDIANAALAA SAVTQVAKVF DQYLNFILE DDMFVLCNQN KELVSYRAIN180
 RPDITTEME TVMDTIVDSL FCFFVTLGAV PIIRCSRGTA AEMVAVKLDK KLRENLRDAR240
 NSLFTGDTLG AGQFSFQRPL LVLVDRNIDL ATPLHHTWTY QALVHDVLDL HLN RVNLEES300
 SGVENSPAGA RPKRKNKKS Y DLTPVDKFWQ KHKGSPPFEV AESVQQELES YRAQEDEVKR360
 LKSIMGLEGE DEGAISMLSD NTAKLTSAVS SLPELLEKKR LIDLHTNVAT AVLEHIKARK420
 LDVYFEYEEK IMSKTTLDKS LLDIISDPDA GTPEDKMRLF LIYYISTQQA PSEADLEQYK480
 KALTDAGCNL NPLQYIKQWK AFTKMASAPA SYGSTTTKPM GLLSRVMNTG SQFVMEGVKN540
 LVLKQQNLPV TRILDNLMEM KSNPETDDYR YFDPKMLRGN DSSVPRNKNP FQEAIVFVVG600
 GGNYYIEQNL VDYIKGKQKG HILYGCSELF NATQFIKQLS QLGQK 645

(2) INFORMATION ON SEQ ID NO. 217:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 101 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

GAGPSQLRLH YPRISMAVRQ WVIALALAA LVVDRVPVA AGKLPFSRMP ICEH MVESPT 60
 CSQMSNLVCG TDGLTYTNEC QLCLARIKTK QDIQIMKDGK C 101

(2) INFORMATION ON SEQ ID NO. 218:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 123 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

QLGWIFYFMS YPLHAHHCSP ADTSWLEVLL WDQHLPSFMI WMSCLVFIRA KQSWHSFVYV 60
 SPSVPQTRLD IWEQVG DSTM CSQM GILEKG SFPATGTSL STTRRAAKAR AITHWRTAML120
 ILG 123

(2) INFORMATION ON SEQ ID NO. 219:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 64 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

IKAKENLNAF FFFFLLRSEI GTVILSTERQ TIKWAMKGGG KVL SIVRGIQ PEIKPIYKHV60
 CSSK 64

(2) INFORMATION ON SEQ ID NO. 220:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 67 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

SFAIPFPWHC TISPIIGQSL GFLGFTMVAT TIRLIDGSNL KKKVMVMDKI SRSREVCYHK60
ITVASTS 67

(2) INFORMATION ON SEQ ID NO. 221:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 117 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

TIISITDSQ LQEVAEQLEI FAALHEVLHI INDRKNLKGQ LQEVAEQLEL ERIGPQHQAQ 60
SDSLTGMAF FKMREFFED HIDDAKYCGH LYGLGSGSSY VQNGTGNAYE EEANKQS 117

(2) INFORMATION ON SEQ ID NO. 222:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 196 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

PTCPIQHFIM MKLWVPSRSL PNSPNHYRSF LSHTLHIRYN NSLFISNTHL SRRKLRVTNP 60
IYTRKRSINI FYLLIPSCRT RLILWIIYIY RNLKHWSTST VRSHSHSIYR LRPSMRTNII120
LRCHSYKPP ISHPYWNPN SRMNLRLLS RQSHLDPIR FPLHLTIYYR GPSNRSPLP180
PRNRIKQPNR IKLRCR 196

(2) INFORMATION ON SEQ ID NO. 223:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 174 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

LPSAIEGPTP VSALLHSSTI VVAGIFLLVR FHPLTTNNNF ILTTILCLGA LTTLFTAICA 60
 LTQNDIKKII AFSTSSQLGL IIVTLGINQP HLAFLHICTH AFFKAILFIC SGSIHSLAD120
 EQDIRKIGNI TKIIPFTSSC LVIGSLALTG IPFLTGFYSK DLIIEAINTC NTNA 174

(2) INFORMATION ON SEQ ID NO. 224:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 123 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

FLKTTALIIS VLGFLIALEL NNLTIKLSIN KANPYSSFST LGFFPSIIH RITPIKSLNL 60
 SLKTSLTLLD LIWLEKTIPK STSTLHTNIT TLTTNQKGLI KLYFISFLIN IILIIILYSI120
 NLE 123

(2) INFORMATION ON SEQ ID NO. 225:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 129 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

NMLLAEVRI\$ MVIRNSVRYL MNRLMFGSEC IYHEENCIID HVTKRATDVN RIEKKSVLKL 60
ILSSIEFMVT QCQVVIIYSI LLWKNINRGK RLIMKENLID VVVYSGKLMC LIRFDIEIRI120
GDSRRMKIK 129

(2) INFORMATION ON SEQ ID NO. 226:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 83 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

FFFFFFFAIQ MNVYFLNPHR VRAELRDAWH SISHPGSLPR SFFFAGSILD LYHFLQRQYP60
EWQSQVYFKV GVFSGSRGDW IPS 83

(2) INFORMATION ON SEQ ID NO. 227:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 122 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

SMMLFKVLVI TVFCGLTVAF PLSELVSINK ELQNSIIDLL NSVFDQLGSY RGTKAPLEDY 60
 TDDDLSTDSE QIMDFTPAAN KQNSEFSTDV ETVSSGFLEE FTENTDITVK IPLAGNPVSP120
 TS 122

(2) INFORMATION ON SEQ ID NO. 228:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

TSTTVFFFPF HSLPVGCTV CSHALCINIL EIYRSVLYFL YCWILIIKTF TRVLNKSSLT60
 RK 62

(2) INFORMATION ON SEQ ID NO. 229:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ARPCMNSTKA LPHGREHTRL KMLSYLKNKM CKSSGWHKTK VNASWGTF LR GLAECVNIID60
 FCLOYMTSVT SLKICTIQFQ LWITSVDLCE GFYLCRMGV 99

(2) INFORMATION ON SEQ ID NO. 230:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

GELQKSSHYH PPFLFEMIFF VHFSGSIGGR IYYNMDHLYF CIYLFITRPQ PQSSFSPTS60
LCL 63

(2) INFORMATION ON SEQ ID NO. 231:

(i) **SEQUENCE CHARACTERISTIC:**

(A) LENGTH: 64 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

INKYRSRDDP YYSIFYHQYC SQNVQKKSFQ ITQEDDNGWT FVIHLKDCGR ANSTHCIVCA60
YGGGL 64

(2) INFORMATION ON SEQ ID NO. 232:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 88 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

PLFCAILKTC TFYFSDSLTF LIECVLYHAV MLWYYSYRVL PILKTCHFVK RSFDSALEVL60
HKLKSLSNIN MKGGTGCNIY SOVTSLYI 88

(2) INFORMATION ON SEQ ID NO. 233:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

```

ASTIMDLLFG RRTPEELLR QNQRALNRAM RELDRERQKL ETQEKKIAD IKKMAKQGQM 60
DAVRIMAKDL VRTRYVRKF VLMRANIQAV SLKIOTLKSNS NSMAQAMKGV TKAMGTMNRQ120
LKLPIQKIM MEFERQAEIM DMKEERIELL HLMIPWVLGK F 161
  
```

(2) INFORMATION ON SEQ ID NO. 234:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```

RRVRTKSFAM MRTASIWPCL AIFLMSAMIF FSWVSSFCRS RSSSRMARFR ALWFCRSSSS 60
GVFRRPNNRS MMVEAHWQAG AGTDTRFRFR VTLLFLGSPT CPPTKAPRSC RRRRRFRGRV120
  
```

(2) INFORMATION ON SEQ ID NO. 235:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

KLPQNPRDHQ MQQFNPLLLH IHDLCPLKL HHDLLDLGQL QLSVHGAGHL GDTLHGLCHR 60
VVGLECLDLE GHSLDVGPHQ YKLAHIAPGA HQVFCHDANS IHLALLGHLL NVCNDFLLLG120
L 121

(2) INFORMATION ON SEQ ID NO. 236:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 180 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

KTKRSVKDAA KKGQKDVCI V LAKEMIRSRK AVSKLYASKA HMNSVLMGMK NQLAVLRVAG 60
SLQKSTEV MK AMQSLVKIPE IQATMRELSK EMMKAGIIEE MLEDTFESMD DQEEMEEAE120
MEIDRILFEI TAGALGKAPS KVTDALPEPE PPGAMAASED EGEEEEEAL EA MQSRLATLRS180

(2) INFORMATION ON SEQ ID NO. 237:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 111 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

LMPFQSQNLQ ERWLPQMRG RKRRLWRPCS PGWPHSAARG CLPRWVCTHS SQELPFYVSL 60
ALHLCCEDYH FGEGSVCLFS FSAQVLGSQR DCSYKSGINK CIIFRKKKK K 111

(2) INFORMATION ON SEQ ID NO. 238:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 103 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

KICERCCQEG PEGCLHSSGQ GDDQVKEGCE QAVCIQSTHE LSAHGDEEPA RGLASGWFFA 60
 EEHRSDDEGHA KSCEDSRDSG HHEGVVQRND EGWDHRGDVR GHF 103

(2) INFORMATION ON SEQ ID NO. 239:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 351 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

TWCTTTMLAA RLVCLRTLPS RVFHPAFTKA SPVVKNSITK NQWLLTPSRE YATKTRIGIR 60
 RGRGQELKE AALEPSMEKI FKIDQMGRWF VAGGAAVGLG ALCYYGLGLS NEIGAIEKAV120
 IWPQYVKDRI HSTYMYLAGS IGLTALSAIA ISRTPVLMNF MMRGSWVTIG VTFAAMVGAG180
 MLVRSIPYDQ SPGPKHLAWL LHSGVMGAVV APLTILGGPL LIRAAWYTAG IVGGLSTVAM240
 CAPSEKFLNM GAPLGVGLGL VEVSSLGSMF LPPTTVAGAT LYSVAMYGGL VLFSMFLLYD300
 TQKVIKRAEV SPMYGVQKYD PINSMLSIYM DTLNIFMRVA TMLATGGNRK K 351

(2) INFORMATION ON SEQ ID NO. 240:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 147 amino acids
- (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

RVAPATVVG RNI DPNEDTK TRPRPTPRGA PMFRNFSLGA HMATVERPPT MPAVYHAALM 60
RRGPPNIVRG ATTAPITPEC SNQARCFGPG LWSYGIDRTS IPAPTMAAKV TPIVTQEPLI120
MKFMRTGVLL IAMADKAVKP ILPAKYI 147

(2) INFORMATION ON SEQ ID NO. 241:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 196 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

KARRRGTM AA AADERSPEDG EDEEEEEQLV LVELSGIIDS DFLSKCENKC KVLGIDTERP 60
ILQVDSCVFA GEYEDTLGTC VIFEENVEHA DTEGNNKTVL KYKCHTMKKL SMTRTLLTEK120
KEGEENIGGV EWLQIKDNDF SYRPNMICNF LHENEDEEVV ASAPDKSLEL EEEEIQMNHR180
FKPGFVEPGE PIAPWE 196

(2) INFORMATION ON SEQ ID NO. 242:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 156 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

PPAPALRHRE TRRPVASLHV GTGALGARSH PPAGSRHLEF WQKQFARRGA DGQEPNKLLR 60
 LGAEARTQDG GSGRAWPVTR RRGAA GPWRR RRTSGVQRTE KTRKRRSSWF WWNYQELLIQ120
 TSSQNVKINA RFWALTLRGP FCKWTA VSL L GSMKTL 156

(2) INFORMATION ON SEQ ID NO. 243:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 132 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

RRLEVS YRQH HFRVSLAPWS KMADEATRRV VSEIPVLKTN AGPRDRELWV QRLKEEYQSL 60
 IRYVENNKNA DNDWFRLESN KEGTRWFGKC WYIHDLLKYE FDIEFDIPIT YPTTAPEIAV120
 PELDGKTAKM YR 132

(2) INFORMATION ON SEQ ID NO. 244:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 159 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

LFAISYSVLP VHLCCLSIQL RNCNFWGSSR ICDRNVKLDV KLIFQEVMDI PAFSKPPSSF 60
 LVGLQSEPIV VSILVVLHIP DKGLIFLLQS LHPQLTISGS GVS LQHRDLR HNTSRGFIRH120
 LGPGRKRNAE VVLPVAYLKA PSSLLWEDET LGCCKTSFE 159

(2) INFORMATION ON SEQ ID NO. 245:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

ATLPDALPPA TKFFLKAFDD SLPSPIQSYL YIFAVFPSSS GTAISGAVVG YVIGMSNSMS 60
 NSYFRRSWIY QHFPNHRVPS LLDSSRNQSL SAFLLFSTYR IRD 103

(2) INFORMATION ON SEQ ID NO. 246:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 285 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

AVRRRGALSL SVGAACGLVA LWQRRRQDSG TMSGFSTEER AAPFSLEYRV FLKNEKGQYI 60
 SPFHDIPIYA DKDVFHVVVE VPRWSNAKME IATKDPLNPI KQDVKKGKLR YVANLFPYKG120
 YIWNYGAIPO TWEDPGHNDK HTGCCGDNDP IDVCEIGSKV CARGEIIGVK VLGILAMIDE180
 GETDWKVIAI NVDDPDAANY NDINDVKRLK PGYLEATVDW FFRYKVPDGG PENEFAFNAE240
 FKDKDFAIDI IKSTHDHWKA LVTCKTNGKR IMLIVQLFVG PLKVC 285

(2) INFORMATION ON SEQ ID NO. 247:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

TKGLRIAQAQ LCPGSPRCRS QSISRRACAL CLRPSTQPNT TYLRKPGGRK RAVGHKSPAE60
TRVPASVQRS QPPRAHRKSC LASLGLCKNN KCLS 94

(2) INFORMATION ON SEQ ID NO. 248:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 113 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

DPRPSRIQHI SGNPAGASER LAIRAQLKRE YLLQYNDPNR RGLIENPALL RWAYARTINV 60
YPNFRPTPKN SLMGALCGFG PLIFIYYIHK TERDRKEKLI QEGKLDRTFH LSY 113

(2) INFORMATION ON SEQ ID NO. 249:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 98 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

VFRSGSEIRI DIYCSCIGPT KQGRIFDEPS AVGIVVLKQV LSFQLGSYGQ PLACARRVSG60
DMLYSAGSRV SGRVRRLDGL YFGNDILANQ GTIAPARF 98

(2) INFORMATION ON SEQ ID NO. 250:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 158 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

TQVMVQSMFA PTDTSDMEAV WKEAKPEDLM DSKLRVCFEL PAENDKPHDV EINKIISTTA 60
 SKTETPIVSK SLSSSLDDTE VKKVMEECKR LQGEVQRLRE ENKQFKEEDG LRMRTVQSN120
 SPISALAPTG KEEGLSTRLL ALVVLFFIVG VIIGKIAL 158

(2) INFORMATION ON SEQ ID NO. 251:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 112 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

VNKALPFISK ALGQSVNTRL SLMTSTSDAA TVQFLWASDS VHQSQGADGL DRTEDESSL 60
 GREWATWGLL CGADRTPOHA GLQLPKGQHQ QARKGVILRE VIQHHVPRPT NV 112

(2) INFORMATION ON SEQ ID NO. 252:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 135 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

SKGCSITETV TVDPGSIIP LGLTQYRRGA VVFTLKHTFL SDGFRNLRFV VTTSVKGPLN 60
LRSVGGSRTR ICSSSPWPLR RTPSERQRRR GGGLLAGGGG RWREGRGSEF ASLLFLVRLC120
STTFLCWQIC FQIDF 135

(2) INFORMATION ON SEQ ID NO. 253:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 189 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

SMQSAVSFFF FSLDQKKICL PTISLVVWPT VTIFLCVQRH IGFAFNDLLR LENTIKTNCS 60
ATGQVVYYQI ITSRCQLHIE SFMKFINKEL FFLCGFNKSS RIVQSLVNVI LIPLNFICCI20
CYLLKYDLFR LLIPLIQEMP RGIPWNGAS YSVNFSSTF ANIMAEFFLS LVRQLLTEFF180
ILTILSHGI 189

(2) INFORMATION ON SEQ ID NO. 254:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 300 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

KSIWKQICQH KNVVEQSLTR KRRDANSPL PSRHRPPPPA SKPPPALRCL SDGVRLRGHG 60
EDEQILVLDL PDLKFKGPF TDVVTNLKL RNPSDRKVCF KVKTTAPRRY CVRPNSGIID120
PGSTVTVSVM LQPFDYDPNE KSKHKFMVQT IFAPPNTSDM EAVWKEAKPD ELMDSKLRCV180
FEMPENNDKL NMEPSKAVP LNASKQDQPM PKPHSVSLND TETRKLMEEC KRLQGEMMKL240
SEENRHLRDE GLRLRKVAHS DKPGSTSTAS FRDNVTSPLP SLLVVIAAIF IGFFLGKFI300

(2) INFORMATION ON SEQ ID NO. 255:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 247 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

GSSGSRFEVV VVLEERRGGR GRGMGRGDGF DSRGKREFDR HSGSDRSLK HEDKRGGSGS 60
 HNWGTVKDEL TESPXYIQKQ ISYNYSDLQ SNVTEETPEG EEHHPVADTE NKENEVEEVK120
 EEGPKEMTLD EWKAIQNKDR AKVEFNIRKP NEGADGQWKK GFVLHKSSE EHAEDSVMD180
 HHFRKPANDI TSQLEINFGD LGRPGRGGRG GRGGRGRGGR PNRGSRTDKS SASAPDVDDP240
 EAFPALA 247

(2) INFORMATION ON SEQ ID NO. 256:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 69 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

FVFDSSPVVR SATSTFVLVL QARSITSTMP IKFTFATRIK SISSAHSTST APSTLFQDHH60
 DLESRAARA 69

(2) INFORMATION ON SEQ ID NO. 257:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 220 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(vi) ORIGIN
(A) ORGANISM: HUMAN

PGRGSMYDRM RRGGDGYDGG YGGFDDYGGY NNYGYGNDGF DDRMRDGRGM GGHGYGGAGD 60
 ASSGFHGGHF VHMRLPLFRA TENDIANFFS PLNPIRVHID IGADGRATGE ADVEFVTHED120
 AVAAMSKDKN NMQHRYIELF LNSTPGGGSG MGGSGMGGYG RDGMNDQGGY GSVGRMGMCN180
 NYSGGYGTPO GGGYGRGGG GSGGYYGOGG MSGGGWRGMY 220

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1105 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AATGAGCCTG	GTGTTAGATG	AGTTTTACAG	CTCACTCAGG	GTGGTGGGTG	TCTCTGCTGT	60
TCTGGGTACT	GGATTAGATG	AACTCTTTGT	GCAAGTTACC	AGTGCTGCCG	AAGAATATGA	120
AAGGGAGTAT	CGTCCTGAAT	ATGAACGTCT	GAAAAAATCA	CTGGCCAACG	CAGAGAGCCA	180
ACAGCAGAGA	GAACAACCTGG	AACGCCTTCG	AAAAAGATATG	GGTTCGTAG	CCTTGGATGC	240
AGGGACTCCC	AAAGACAGCT	TATCTCCTGT	GCTGCACCCT	TCTGATTGA	TCCTGACTCG	300
ACCAACATTG	GAAGCAGACA	CGGATATCTA	TGCATTGTAC	CACAGAGTTA	CAGAGGAAAG	360
CCATGAAGAG	CGAGCATTCC	AGAATTTTAT	GCAAGAATCG	ATGCACAAT	ACTGGAAGAG	420
AAACAATAAA	TAGGAGACTT	TAGCACACTT	CACTTGTTTC	TAGAAGTCCA	GAATTTTGA	480
CCTCCACGTG	AAAGAACTGT	TCTTACCTCT	GAAGTGGGGG	CTCCATAAG	GGATAATTTT	540
CCTCAGAGTA	GCAAAGTTTC	TCTTATTAGA	GAAATCTTGT	GACTCAGATG	AAGTCAGGGA	600
TAGAAGACCC	TTGGACCTGG	CAGGTTAATG	CTGATTATTC	CTTGGCCTTT	CCCTTGTATT	660
TATGCAAGGA	AGGATAATACT	GAGCTGATAC	TCTTCCAAGC	CTACAACCTC	AAGTTTTATC	720
ATTTGAACCTC	AGTACTTTTT	GCTGCTGAGG	AATGGAATCA	AAAGAACGTA	GTCTCCTGGT	780
AACCACTCA	GATCTCTATT	ATTAGGCTAG	ATGTATAGCC	TCTACTCCCC	CAGCTTCTTG	840
CTCTTGACCC	TGCACTGTAA	GTTGCCCTTC	TATTAGCAGC	CAAGGAAAAG	GGAAACATGA	900
GCTTATCCAG	AACGGTGGCA	GAGTCTCCTT	GGCAATCAAC	CAACGTTGCT	ATGAAATATG	960
CCTCACTACTG	TATAGCTCAT	TATAGGACGT	CAGGTTTGTT	GAAAAAAGTG	GGCAAGACAT	1020
GATTAATGAA	TCAGAATCCT	GTTTCATTGG	TGACTTGAT	AAAGACTTTT	TAATTTTAAA	1080
AAAAA	AAAAA	AAAAA				1105

(2) INFORMATION ON SEQ ID NO. 259:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1088 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

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ATTCCAAACA TGGCGGCTCC ACTAGGGGGT ATGTTTTCTG GGCAGCCACC CGGTCCCCCT 60
CAGGCCCCGC CGGGCCTTCC GGGCCAAGCT TCGCTTCTTC AGGCAGCTCC AGGCGCTCCT 120
AGACCTTCCA GCAGTACTTT GGTGGACGAG TTGGAGTCAT CTTTCGAGGC TTGCTTTGCA 180
TCTCTGGTGA GTCAGGACTA TGTCAATGGC ACCGATCAGG AAGAAATTCG AACCGGTGTT 240
GATCAGTGTA TCCAGAAGTT TCTGGATATT GCAAGACAGA CAGAATGTTT TTTCTTACAA 300
AAAAGATTGC AGTTATCTGT CCAGAAACCA GAGCAAGTTA TCAAAGAGGA TGTGTCAGAA 360
CTAAGGAATG AATTACAGCG GAAAGATGCA CTAGTCCAGA AGCACTTGAC AAAGCTGAGG 420
CATTGGCAGC AGGTGCTGGA GGACATCAAC GTGCAGCACA AAAAGCCCCG CGACATCCCT 480
CAGGGCTCCT TGGCCTACCT GGAGCAGGCA TCTGCCAACA TCCCTGCACC TCTGAAGCCA 540
ACGTGAGCAA AGGGCAGAGG CAGTTGGCCT ATGAGTGGGC TGATGCGTGA GGTGGCCAC 600
ACATTCCTTC CTGTGGACTT GACATTTTGG AAGAACTCTT TGCCAGATAA TGAGTTCATT 660
TTAGTTTTAT GCTCCCATTG AAAAATTTTC CACTATTTTT ATAAGCTGTT AATTTCTTGA 720
GTACTTTATA ACATGTCTGT AGCTTGGATA AACCAAGTAA GTATTTTTTT TTTGTCTTTA 780
GCGAAGTTTA GACTGTGAAT ATGATGACAC AGATTCTTTT TTATGGTGGC TTTGCTTGT 840
TTAAATTTTT GCATGACTTT TCATCTTTTT ATGTGTGTTT CCTGTAGTTT GATCCGAAGG 900
AAAAGAGTAT AGTAGCCTGA GAATCAGGAG ATGGGAGTTT TAGTCGTAGG CCTTATGATA 960
ATTACCCCGC GGTGGTGTGT AGAAAAGTAT GTAAATTTGC TCTGTTTTAA GACTTTGAAC 1020
TACCTCAAGA AGAGGAATCT AATACAATAT TTGTAATGTT AAAAAAAAAA AAAAAAAAAA 1080
AAAAAAAAA

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(2) INFORMATION ON SEQ ID NO. 260:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3292 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

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ATGCCGAAC TCTGCGCTGC CCCCACCTGC ACGCGGAAGA GCACGCAGTC CGACTTGGCC 60
TTCTTCAGGT TCCGCGGGA CCCTGCCAGA TGCCAGAAGT GGGTGGAGAA CTGTAGGAGA 120
GCAGACTTAG AAGATAAAAC ACCTGATCAG CTAAATAAAC ATTATCGATT ATGTGCCAAA 180
CATTTTGAGA CCTCTATGAT CTGTAGAACT AGTCCTTATA GGACAGTTCT TCGAGATAAT 240
GCAATACCAA CAATATTTGA TCTTACCAGT CATTTGAACA ACCCACATAG TAGACACAGA 300
AAAACGAATAA AAGAACTGAG TGAAGATGAA ATCAGGACAC TGAAACAGAA AAAAATTGAT 360
GAAACTTCTG AGCAGGAACA AAAACATAAA GAAACCAACA ATAGCAATGC TCAGAACCCC 420
AGCGAAGAAG AGGGTGAAGG GCAAGATGAG GACATTTTAC CTCTAACCCCT TGAAGAGAAG 480
GAAAACAAAG AATACCTAAA ATCTCTATTT GAAATCTTGA TTCTGATGGG AAAGCAAAAC 540
ATACCTCTGG ATGGACATGA GGCTGATGAA ATCCCAGAAG GTCTCTTTAC TCCAGATAAC 600
TTTCAGGCAC TGCTGGAGTG TCGGATAAAT TCTGGTGAAG AGGTTCTGAG AAAGCGGTTT 660
GAGACAACAG CAGTTAACAC GTTGTTTTGT TCAAAAACAC AGCAGAGGCA GATGCTAGAG 720
ATCTGTGAGA GCTGTATTCG AGAAGAAACT CTCAGGGAAG TGAGAGACTC ACACITCTTT 780
TCCATTATCA CTGACGATGT AGTGGACATA GCAGGGGAAG AGCACCTACC TGTGTTGGTG 840
AGGTTTGTG ATGAATCTCA TAACCTAAGA GAGGAATTTA TAGGCTTCCT GCCTTATGAA 900
GCCGATGCAG AAATTTTGGC TGTGAAATTT CACACTATGA TAACTGAGAA GTGGGGATTA 960
AATATGGAGT ATTGTCGTGG CCAGGCTTAC ATTGTCTCTA GTGGATTTTC TTCCAAATG1020
AAAGTTGTTG CTTCTAGACT TTTAGAGAAA TATCCCCAAG CTATCTACAC ACTCTGCTCT1080
TCCTGTGCCT TAAATATGTG GTTGGCAAAA TCAGTACCTG TTATGGGAGT ATCTGTTGCA1140
TTAGGAACAA TTGAGGAAGT TTGTTCTTTT TTCCATCNGA TCACCACAAC TGCTTTTAGA1200
ACTTGACAAC GTAATTGCTG TTCTTTTCA GAACAGTAAA GAAAGGGGTA AAGAACTGAA1260
GGAAATCTGC CATTCTCAGT GGACAGGCAG GCATGATGCT TTTGAAATTT TAGTGGAACT1320
CCTGCAAGCA CTTGTTTTAT GTTTAGATGG TATAAATAGT GACACAAATA TTAGNATGGG1380
AATAACTATA TAGCTGGCCG AGCATTNNGT ACTCTGCAGT GCAGTGCAG ATTTTGATT1440
CATTGTTACT ATTGTTGTTC TTAATAATGT CCTATCTTTT ACAAGAGCCT TTGGGAAAAA1500
CCTNCCANGG GGCAACCTC GTGATGTCTT CTTTGGCGCC GGTAGCTTGA CTNGCAGTAC1560
TGNNCATTCA CNTCAACGAA GTGAGTGGGA AAATATTNGA AGTTTATCAT GAATTTTGGT1620
TTGAGGAAGC CACAAATTTG GCAACCAAAC TTGATATTCA AATGAAACTC CCTGGGAAAT1680
TCCGCAGAGC TCACCNAGG GTAACCTGGA ATCTCAGCTA ACNCTCTGAG AGTTACTATA1740
AAGAAACCCN TAAGTGTCCC AACAGTGGAG CACATTATTC AGGAACCTAA AGATATATTC1800
TCAGAACAGC ACCTCAAAGC TCTTAAATGC TTATCTCTGG TACCCTCAGT CATGGGACAA1860
CTCAAATTCA ATACGNTCNG GAGGAACACC ATGCTGACAT GTATAGAAGT GACTTACCCA1920
ATCCTGACAC GCTGTCAGCT GAGCTTCATT GTTGGAGAAT CAAATGGAAA CACAGGGGGA1980
AAGATATAGA GCTTCCGTCC ACCATCTATG AAGCCCTCCA CCTGCCTGAC ATCAAGTTT2040
TTCCTAATGT GTATGCATTG CTGAAGGTCC TGTGTATTCT TCCTGTGATG AAGGTTGAGA2100
ATGAGCGGTA TGAAAATGGN ACGAAAGCGT CTTTAAAGCA TATTTGAGGG AACACTTTGA2160
CAGACCCAAA GGTCAAGTAA CTTGGCTTTT GCTTTAACAT AAATTTTGGA TATTTAAACA2220
CGACCTGGAT TTAATGGTGG ACACATATAT TAAACTCTAT ACAAGTAAGT CAGAGCTTCC2280
TACAGATAAT TCCGAAACTG TGGNAAAATA CCTAAGAGAC TTTTAAAAAT AGGCTTCTT2340
ATATTTGATA TTTGGAAGAA AAAGCCGTAA GGTGTATGTA GACCACTTAA TCACTAAATA2400
TCTTTGCCCN TAGGACTCCA TTGAATACAT TAGCCATTGA TAATCTACCT GTTTAAATGG2460
CCCCTGTTG AACTCTCAAG CTTTGAAGAC CTACCTGTTT TTCCAGAAGA GAACGTTGAA2520
AGTGCCATGT TTCCNTTTTG CGTGATCTCT GTTGATGGCA CTCTGGAATT GTTTCAGTTA2580
AGTCATTTTA GACATAGCAT TTATTATCAC TGTGGNATCT CTAATTGTTG GGTGTTATGA2640
ATTCTTTGNA AGNAAATATA TTTTNGAAGA GGTGTGGGNA GGNAAGGAAT ACNATTTTAT2700
NAAAATGTTG TAGTGNAAGN CCCACAATTN GACCTTTNGA CTAATANGGA GTTTTAAGTA2760
TNGTTAAAAA TNCTATACTG GNNACAGNTT ACAAGAAATT ACCGGAGAAA AGCTTGTGAG2820
CTCACCNAAA CAAGGNATTT NCAGTGTAGA TTTTGTCTNT TCTTGAACNT TNAAAGAAAN2880
CAAATGANCA AAGTTTGAAT NGGAAAAGCC TGCTGTTGTT CCNACATCTC NGTTGCTGTT2940
NNTACANTTC CNNTTTGTG GAGNCCTACN ATCTTNCCTA AGCTTTTNA GCANGGTATA3000

TNGTTGAACA CTTCNGTTT CATGGTTGAG ACAGAATCAG AGGCCATGGA TACTGACAAC3060
TGATTGTCT GTTTTTTTC TCTGTCTTN TTCCATGACT CTTATATACT GCCTCATCTT3120
GATTTATAAG CNAAAANCCT GGANAAACCT ANCAAAATAA GTGTTGTGGT TTATCTAGAA3180
AAATATGGAA AATATTGCTG TTATTTTGG TGAAGAAAT CNAATTTTGT ATAGTTTAT3240
TCAATCTAAA TAAAATGTGA ATTTTGTTTA AAAAAAAAAA AAAAAAAAAA AA 3292

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(2) INFORMATION ON SEQ ID NO. 261:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1196 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

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GGTAGAAAAT GCAATAAATT CTGGGACAAT GCCCAGACCT CTGGCATAGA GGAGCCTTCT 60
GAGACAAAGG GTTCTATGCA AAAAAGCAAA TTCAAATATA AGTTGGTTCC TGAAGAAGAA 120
ACCACTGCCT CAGAAAATAC AGAGATAACC TCTGAAAGGC AGAAAGAGGG CATCAAATTA 180
ACAATCAGGA TATCAAGTCG GAAAAAGAAG CCCGATTCTC CCCCCAAAGT TCTAGAACCA 240
GAAAACAAGC AAGAGAAGAC AGAAAAGGAA GAGGAGAAAA CAAATGTGGG TCGTACTTTA 300
AGAAGATCTC CAAGAAATATC TAGACCCACT GCAAAAGTGG CTGAGATCAG AGATCAGAAA 360
GCTGATAAAA AAAGAGGGGA AGGAGAAGAT GAGGTGGAAG AAGAGTCAAC AGCTTTGCAA 420
AAAAGTGACA AAAAGGAAAT TTTGAAAAAA TCAGAGAAAG ATACAAATTC TAAAGTAAGC 480
AAGGTAAAAA CCAAAGGCAA AGTTGCATGG ACTGGTTCTC GGACACGTGG CAGATGGAAA 540
TATTCCAGCA ATGATGAAAG TGAAGGTCT GGCAGTGAAA AATCATCTGC AGCTTCAGAA 600
GAGGAGGAAG AAAAGGAAAG TGAAGAAGCC ATCCTAGCAG ATGATGATGA ACCATGCAAA 660
AAATGTGGCC TTCAAACCA TCCTGAGCTA ATTCTTCTGT GTGACTCTTG CGATAGTGGA 720
TACCATACTG CCTGCCTTCG CCCTCCTCTG ATGATCATCC CAGATGGAGA ATGGTTCTGC 780
CCACCTTGCC AACATAAACT GCTCTGTGAA AAATTAGAGG AACAGTTGCA GGATTTGGAT 840
GTTGCCTTAA AGAAGAAAGA GCGTGCCGAA CGAAGAAAAG AACGCTTGGT GTATGTTGGT 900
ATCAGTATTG AAAACATCAT TCCTCCACAA GAGCCAGACT TTTCTGAAGA TCAAGAAGAA 960
AAGAAAAAAG ATTCAAAAAA ATCCAAAGCA AACTTGCTTG AAAGGAGGTC AACAAGAACA1020
AGGAAATGTA TAAGCTACAG ATTTGATGAG TTTGATGAAG CAATTGATGA AGCTATTGAA1080
GATGACATCA AAGAAGCCGA TGGAGGAGGA GTTGGCCGAG GAAAAGATAT CTCCACCATC1140
ACAGGTCATC GTGGGAAGA CATCTCTACT ATTTTGGATG AAAAAATAAT AACGGC 1196

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(2) INFORMATION ON SEQ ID NO. 262:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1467 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

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AAGGACGCTT GCCTTTTTC GGTGCGGGAA GGGGGAAGAA GGTAACCTCC GGTGACGGGG 60
TTGCATCACT TCCTCTCAAG CTGCGGCGTT TGTGTTGGTGG GGTACACGC GGGTTCAACA 120
TGCCTATCGA AAAGTGTTAT TTCTGTTCCG GGCCCATCTA TCCTGGACAC GGCATGATGT 180
TCGTCCGCAA CGATTGCAAG GTGTTGAGAT TTTGCAAATC TAAATGTCAT AAAAAGCTTTA 240
AAAAGAAGCG CAATCCTCGC AAAGTTAGGT GGACCAAAGC ATTCCGGAAA GCAGCTGGTA 300
AAGAGCTTAC AGTGGATAAT TCATTTGAAT TTGAAAAACG TAGAAATGAA CCTATCAAAT 360
ACCAGCGAGA GCTATGGAAT AAAACTATTG ATGCGATGAA GAGAGTTGAA GAAATCAAAC 420
AGAAGCGCCA AGCTAAATTT ATAATGAACA GATTGAAGAA AAATAAAGAG CTACAGAAAG 480
TTCAGGATAT CAAAGAAGTC AAGCAAAACA TCCATCTTAT CCGAGCCCCT CTTGCAGGCA 540
AAGGGAACA GTTGAAGAG AAAATGGTAC AGCAGTTACA AGAGGATGTG GACATGGAAG 600
ATGCTCCTTA AAAATCTCTG TAACCATTTT TTTTATGTAC ATTTGAAAAT GCCCTTTGGA 660
TACTTGGAAC TGCTAAATTA TTTTATTTTT TACATAAGGT CACTTAAATG AAAAGCGATT 720
AAAAGACATC TTTCTGTCAT TGCCATCTAC ATAATATCAG ATATTACGGA TGTAGATTG 780
CATCTCAGTG TTAAATCTTT ACTGATAGAT GTACTTAAGT AAATCATGAA AATTCTACTT 840
GTAACATAG AAGTGAATTG TGGACGTAAA ATGGTTGTGC TATTTGGATA ATGGCACTAG 900
GCAGCATTTG TATAGTAACT AATGGCAAAA ATTCATGGCT AGTGATGTAT AAAATAAAAT 960
ATTCCTTTGCA GTAAAATATT CCCTTTGTTA ATGTTATAGA AGGGGGGATA CAAAAAGGAA1020
CTAACAATTT GATGGCAGT GTCAGATATT TTTATTTTAG TATTTCTGT TTTGGTTTAT1080
TTGCATCTTA GAAGAGCATA ATGACATTGT TTGATGAAGC CTAATTATGC TGGACTGTTT1140
TGACCTGGTT TAACCTTCT GATAGGTAGT TGTGGATGCT GGGGATGAGA ACTGAATAAT1200
CTTTGCCTGG AGTGACACTA CACTCTAGAA TTTCCACTTT GGAGAATACT CAGTCCAAC1260
TTGTGATTCC TGATAGAACA GACTTTACTT TTCTAGCCCA GCATTGATCT AGAAGCAGAG1320
GAATCCCAGC GCCTTTTAAA AGTTGTTATG TGGTTTTCTT TAAAAAGCT CCTGTTTTTG1380
AAAAGTAGAA TTTATGGGTA CAACGTATGT TCATTATTTG TACATAAAAT AAAACCATTT1440
AAAAAGTAAA AAAAAAAAAA AAAAAAC
1467

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(2) INFORMATION ON SEQ ID NO. 263:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 739 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

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CGGCTCGAGC CCCGCTCAGT CACCCGCAGC AGGCGTGCAG TTTCCCGGCT CTCGCGCGCG 60
CCGGGGAAGG TCAGCGCCGT AATGGCGTTC TTGGCGTCGG GACCCTACCT GACCCATCAG120
CAAAAGGTGT TGCGGCTTTA TAAGCGGGCG CTACGCCACC TCGAGTCGTG GTGCGTCCAG180
AGAGACAAAT ACCGATACTT TGCTTGTTTG ATGAGAGCCC GGTTTGAAGA ACATAAGAAT240
GAAAAGGATA TGGCGAAGGC CACCCAGCTG CTGAAGGAGG CCGAGGAAGA ATTCTGGTAC300
CGTCAGCATC CACAGCCATA CATCTTCCCT GACTCTCCTG GGGGCACCTC CTATGAGAGA360
TACGATTGCT ACAAGGTCCC AGAATGGTGC TTAGATGACT GGCATCCTTC TGAGAAGGCA420
ATGTATCCTG ATTACTTTGC CAAGAGAGAA CAGTGGAAGA AACTGCGGAG GGAAAGCTGG480
GAACGAGAGG TTAAGCAGCT GCAGGAGGAA ACGCCACCTG GTGGTCCTTT AACTGAAGCT540
TTGCCCCCTG CCCGAAAGGA AGGTGATTTG CCCCCACTGT GGTGGTATAT TGTGACCAGA600
CCCCGGGAGC GGCCCATGTA GAAAGAGAGA GACCTCATCT TTCATGCTTG CAAGTGAAAT660
ATGTTACAGA ACATGCACTT GCCCTAATAA AAAATCAGTG AAATGGAAAA AAAAAAAAAA720
AAAAAAAAAA AAAAAAAAAA

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739

(2) INFORMATION ON SEQ ID NO. 264:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2146 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

TTTTTTTTTT	TTTTTTTTTT	TCCCAGGCC	TCTTTTTTATT	TACAGTGATA	CCAAACCATC	60
CACCTGCAAA	TTCTTTGGTC	TCCCATCAGC	TGGAATTAAAG	TAGGTACTGT	GTATCTTTGA	120
GATCATGTAT	TTGTCTCCAC	CTTGGTGGAT	ACAAGAAAGG	AAGGCACGAA	CAGCTGAAAA	180
AGAAGGGTAT	CACACCGCTC	CAGCTGGAAT	CCAGCAGGAA	CCTCTGAGCA	TGCCACAGCT	240
GAACACTTAA	AAGAGGAAAG	AAGGACAGCT	GCTCTTCATT	TATTTTGAAA	GCAAATTCAT	300
TTGAAAGTGC	ATAAATGGTC	ATCATAAGCT	AAACGTATCA	ATTAGACCTT	CAACCTAGGC	360
TATTTAATAA	TACACCACAC	TGAAATTATT	TGCCAATGAA	TCCCAAAGAT	TTGGTACAAA	420
TAGTACAATT	CGTATTGGCT	TTCCTCTTTT	CTTCTTCAG	ACAAACACCA	AATAAAATGC	480
AGGTGAAAG	GATGAACCACT	GACCTAGAGG	TGACTTAGAA	ATTTATGCTG	ACTCGATCTA	540
AAAAAAATTA	TGTTGGTTAA	CGTTAACCTA	TCTAAAATCG	GGCCCTTTTCG	GCAAGCCCTT	600
CAAAGGAGGT	CAAGTCACAG	TCATACAGCT	AGAAAAGTCC	CTGAAAAAAA	GAATTGTTAA	660
GAAGTATAAT	AACCTTTTCA	AAACCCACAA	CGCAGCTTAG	TTTTCTTTTA	TTTATTGTG	720
GTCATGAAGA	CTATCCCCAT	TTCTCCATAA	AACCTCTCCT	CCATCTGCT	GCATTATGGC	780
ACAAAAGACT	CTAAGTGCCA	CCAGACAGAA	GGACCAGAGT	TCCGATTAT	AAACAATGAT	840
GCTGGGTAAT	GTCTAAATGA	GAACATTGGA	TATGGATGGT	CAGATGAAAG	CTCGAGCCGA	900
ATTCCGGTCTG	AGCTTTTCATC	TGACCATCCA	TATCCAATGT	TCTCATTTAA	ACATTACCCA	960
GCATCATTGT	TTATAATCAG	AAACTCTGGT	CCTTCTGTCT	GGTGGCACTT	AGAGTCTTTT	1020
GTGCCATAAT	GCAGCAGTAT	GGAGGGAGGA	TTTTATGGAG	AAATGGGGAT	AGTCTTCATG	1080
ACCACAAATA	AATAAAGGAA	AACTAAGCTG	CATTGTGGGT	TTTGAAAAGG	TTATTATACT	1140
TCTTAACAAT	TCTTTTTTCA	GGGACTTTTC	TAGCTGTATG	ACTGTTACTT	AAACTATCTA	1200
AAATAGAGCA	TTTTGGTATC	TTTCTCTGTA	CCATCCATAT	CCAATGTTCT	CATTTAAACA	1260
TTACCCAGCA	TCAATTTGTTA	TAATCAGAAA	CTCTGGTCCT	TCTGTCTGGT	GGCACTTAGA	1320
GTCTTTTGTG	CCATAATGCA	GCAGTATGGA	GGGAGGATTT	TATGGAGAAA	TGGGGATAGT	1380
CTTCATGACC	ACAAATAAAT	AAAGGAAAAC	TAAGCTGCAT	TGTGGGTTTT	GAAGAGGTTA	1440
TTATACTTCT	TAACAATTCT	TTTTTTCAGG	GACTTTTTCTA	GCTGTATGAC	TGTTACTTGA	1500
CCTTCTTTGA	AAAGCATTCC	CAAAATGCTC	TATTTTAGAT	AGATTAACAT	TAACCAACAT	1560
AATTTTTTTT	AGATCGAGTC	AGCATAAATT	TCTAAGTCAG	CCTCTAGTCG	TGGTTCATCT	1620
CTTTCACCTG	CATTTTATTT	GGTGTGTTG	TGAAGAAAGG	AAAGAGGAAA	GCAAAACGA	1680
ATTGTACTAT	TTGTACCAAA	TCTTTGGGAT	TCATTGGCAA	ATAATTTTCAG	TGTGGTGTAT	1740
TATTAAATAG	AAAAAAAAAA	TTTTGTTTCC	TAGGTTGAAG	GTCTAATTGA	TACGTTTGAC	1800
TTATGATGAC	CATTTATGCA	CTTTCAAAATG	AATTTGCTTT	CAAAATAAAT	GAAGAGCAGC	1860
TGTCCTTCTT	TCCTCTTTTA	AGTGTTTCAG	TGTGGCATGC	TCAGAGGTTT	CTGCTGGATT	1920
CCAGCTGGAG	CGGTGTGATA	CCCTCTTTTT	TCAGCTGTTT	GTGCCCTTCCT	TTCTTGATCT	1980
CACCAAAGTG	GAGACAAATA	CATGATCTCA	AAGATACACA	GTACCTACTT	AATTCCAGCT	2040
GATGGGAGAC	CAAGAATTTT	GCAAGTGGAT	GGTTTGGTAT	CACCTGTAAT	AAAAAGAGGG	2100
CCTGGGAATT	CTTGCGATTTC	CATCTCTAAA	AAAAAAAAAA	AAAAAA		2146

(2) INFORMATION ON SEQ ID NO. 265:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```

CAAGTAAATG CAGCACTAGT GGGTGGGATT GAGGCTATGC CCTGGTGCAT AAATAGAGAC 60
TCAGCTGTGC TGGCACACTC AGCGGCTCTG GACCGCATCC TAGCCGCCGA CTCACACAAG 120
GCAGGTGGGT GAGGAAATCC AGAGTTGCCA TGGAGAAAAT TCCAGTGTCA GCATTCTTGC 180
TCCTTGTTGGC CCTCTCCTAC ACTCTGGCCA GAGATACCAC AGTCAAACCT GGAGCCAAAA 240
AGGACACAAA GGACTCTCGA CCCAACTGC CCCAGACCCT CTCCAGAGGT TGGGGTGACC 300
AACTCATCTG GACTCAGACA TATGAAGAAG CTCTATATAA ATCCAAGACA AGCAACAAAC 360
CCTTGATGAT TATTCATCAC TTGGATGAGT GCCCACACAG TCAAGCTTTA AAGAAAGTGT 420
TTGCTGAAAA TAAAGAAATC CAGAAATTGG CAGAGCAGTT TGTCCTCCTC AATCTGGTTT 480
ATGAAACAAC TGACAAACAC CTTTCTCCTG ATGGCCAGTA TGTCCCCAGG ATTATGTTTG 540
TTGACCCATC TCTGACAGTT AGAGCCGATA TCACTGGAAG ATATTCAAAC CGTCTCTATG 600
CTTACGAACC TGCAGATACA GCTCTGTTGC TTGACAACAT GAAGAAAGCT CTCAGTTGTC 660
TGAAGACTGA ATTGTAAAGA AAAAAAATCT CCAAGCCCTT CTGTCTGTCA GGCCTTGAGA 720
CTTGAAACCA GAAGAAGTGT GAGAAGACTG GCTAGTGTGG AAGCATAGTG AACACACTGA 780
TTAGGTTATG GTTTAATGTT ACAACAATA TTTTAAAGA AAAACAAGTT TTAGAAATTT 840
GGTTTCAAGT GTACATGTGT GAAAACAATA TTGTATACTA CCATAGTGAG CCATGATTTT 900
CTAAAAAAA AAATAAATGT TTTGGGGGTG TTCTGTTTTC TCCAAAAAAA AAAAAAAA 960
AAAAAAA AAAAATAATGCC CCCAAGGGGA CGGGTTACAA TTGGGGGGCG1020

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(2) INFORMATION ON SEQ ID NO. 266:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1652 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

AATTCGGATC	CATGGGCCAC	AGTGGATGGC	TTGAAATGTG	GCTGAGCGCT	TCGGACAATT	60
CGGATCCATG	NNNNGTGGCC	ACCCCAAGAC	GCGCCCCAGC	CCGCCATGGC	CCGGATCCTN	120
NCCGGGNNTC	CTGCCTTCTG	TCCCTGCTCC	TGGCCGGNGT	TTGTTCCGCC	GGGCCGGGGA	180
CAAGAGAAGT	CTAAGACAGA	CTGCCATGGC	GGTNATGAGT	GGTACCATCT	ACGAGTATGG	240
AGCCCTCACC	ATCGATGGGG	AGGAATACAT	TCCTTTTAAG	CAGTATGCAG	GCAAATATAT	300
CCTCTTTGTC	AACGTAGCCA	GCTACTGAGG	TCTGACAGAC	CAATACCTTG	AACTGAATGC	360
ACTACAAGAA	GAACCTGGGC	CATTTGGCTN	TGGTCATTCT	GGGCTTCCCT	TCCAACCAAT	420
TTGGCAAACA	GGAGCCAGGC	GAGAACTCGG	AGATACTCCC	CAGTCTCAAG	TATGTTTCGNN	480
ACCAGGTNNG	GGGGCTTTGT	GNCCTAATTN	NNNTCCAGNC	TCNTTTGAGA	AANNGGANGA	540
TNGTNGAACN	GGGGAGNAAA	GAGCNAGAAA	TTCTACACTT	TCCTGAAGAA	CTCCTGCCCT	600
CCCACTGCAG	NAACTCCTGG	GNCTCANCCT	GGCCGCNCTC	TTTTGGGAAC	CCATGAAGAT	660
CCATGACATN	CCGCTGGAAC	TTTGAGAAGT	TCCTGGTNGG	GGCCNAGANT	GGCATACCGG	720
TTATGCGCTG	GTACCACCGG	ACCACAGTCN	AGCAACGTCN	AAGATGGACA	TCCTGNTCNT	780
TACATGAGGC	GGCAGGCANG	CCCTGANGCG	CCNAGGGGGN	AAGTAACTGA	NTGCCNNNC	840
CACCCCTACCC	CTACCCCTCG	CCCATCATNG	CAAGGGCCGA	NGGAGGGGCT	CTTNCAGGAA	900
GGAAGCCACA	TTCCCAGTCA	TTCTNANCCC	CCACCCCA	TTCTCTTNC	TTNATTACAT	960
AAAAGACAAG	CCNTGGCACA	ACTGTGTGTC	TGAACCACTG	TNGGACACGT	GACAATTGTN	1020
CCCAGTGTGT	GCATGGCTAC	ACAGNCCACG	TATCTGCCTG	CNTTGAAACC	CANGGGNATG	1080
GTCCATCNTG	TNGTTTACGG	NCTTGGCACA	ACACCCNNTC	ATATTTTTTT	CAGCNTTTCT	1140
GTTCCAAANN	TGAGNNCCCA	AANNGGAAAC	ACNAANGTTC	TNAGGTCCNA	ATNGGTTCTG	1200
CTCAAANCCN	TGANACATNC	ATTCNTTGGG	GNCCANGCAT	CNTCCACAT	NGCCACACN	1260
TACACACCAC	CNAGCCTCCT	TCTTCTTNC	CTGNAAGGAC	CCNTCCNNNN	TGAGCCCCCA	1320
AGCCNCATCC	CACAGTGCNT	CCTGAGACCA	GCCAAGACAA	CTGTGAGCGC	GATGGCCGTG	1380
TANCCCCAGG	TNCAGGGGNT	GGTGTCTCTA	TGAAGGANNG	GGNNCCCGNA	AGCCCTTGNT	1440
GGGNCGGNGC	CTCCCCCTGAG	CCCNGTCTGT	GGTGCCNAGC	CCTTAGTGCA	TTCAGGCTTA	1500
GGCTCCCNAG	GCANGGGACA	CTACCCCCGC	GCCTCTGGAG	GACATGCTAT	CCTCTCACTC	1560
TGTCCACTGG	TATCTCAACA	CCCCCATCTG	CCCAGTAAAG	GTCTTTCTGA	AGCAAAAAAA	1620
AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	GG			1652

(2) INFORMATION ON SEQ ID NO. 267:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1409 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

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GGAGTGGCCC TCTGTGAGGG GCTCAAATGG TTGCAATTCA TGGCGCGTTA CGACTTGGCT 60
CACTTAATCA AATCCCTACC AACTCTAACT TGCCGAAGGA AGAACTTGAC CTCTTGGAGA 120
ACCCTCGATT GGTTTTTCCT GCCATTTAGA TGTTGAAGTA CCCCATGAAG AGCTGCAAAA 180
ATTCTCAAAG GTGGATTACA GGAGGTGGCA GAACAGTTAG AGCTGGAACG GATAGGACCA 240
CAACATCAGG CAGGATCTGA TTCATTGCTC ACAGGAATGG CCTTTTCAA AATGAGAGAA 300
ATGTTCTTTG AAGATCATAT TGATGATGCC AAATATTGTG GTCATTGTA TGGCCTTGGT 360
TCTGGTTCAT CCTATGTACA GAATGGCACA GGAATGCAT ATGAAGAGGA AGCCAACAAG 420
CAGTCATGAC ATGAAATAGT CCTTTTATTT TTATTTGAG CTACACACAT GCTTGTATAT 480
AGGTTTTATC TCTGGTTGAA TCCCTCGAAC AATAGACAGT ACCTTTCCCC CCCCTTTCAT 540
GGCCCATTTT ATTGTCTGCC TTTCAGTACT AAGTATGACC GTTCCTATCT CAGATCTTAA 600
TAAAAAGAAA AAAAAAAGCG CATTGAGGTT AAATTTGGCC TTAATTTAAT ATACTTGTTA 660
GCAAGCGTGT GTGACAGAGA GTGGGGGAAAG CTACATCATT GAATATTTG ATAAACTTTA 720
CCGACTTGAG TTTGGTTTAT TTTTCCCTTT TCCTAAATTA ACTAGCACTG ACTGTAATTT 780

ATTTCCTGT TTCACGTCTC TCCCTTCCAT TCTGCAGGAG TTTTAGCTAT TTGAGATCGT 840
GGACCATCAG TTTTGCACCT TAGAGAGTGT TTCTGACTCT AAACCTGTTT TATCAGAAAA 900
TTTGTTTTTT CTTGATCTTA GCTGGAAAAA TCTGCCAACT TTACACAGTA TTTACTTGGT 960
TTTGACCCAC AGAATATAGC ACGTTGTGCA AACTGTGCGT TCAGCGAAAC TTAAGAAAGA 1020
CAAGAAACTA CTGAGGAGCT TAGTAAGTGC TGTCTCTGTA CGTAGTGTTT AATCTTCCAA 1080
GCACATCTAG TGTCTGTCAG TTTCTAATTG GCATGTGTAG GCTGCTCTGT GACTGAAGAA 1140
TTTTCAAACC AGCTTTACAC CCTTCAGGAA AAATCCCTGT GATTGGATGG TTACTATCTG 1200
CCAGGAACTG GTACCCAGAT GTGAAGCACA GTTATTATGA TAGACACTTC CTGAGTGCTA 1260
TTGTATCCAC ACCATTACCT TTTTTTTTAA ATTGGAGCCA TCTATGAGCC TGATTGTGGT 1320
CGCAACCATT GTAAAACCCA GAAAGCCTAG GGATTGGCCA ATAATTGGGG AAATGGTGCA 1380
GTGCCAAGGA AATGGGATGG CAAAAGAAG

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(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

CCACGCGTC	CCGGAACGG	CGGCGCGGC	GACAGGACG	AGGGGCTTA	GTTGGTGGGC	60
AAGTCGGGGA	TCCCAGAAAG	AGAAGCGTGA	CCCGGAAGCG	GAAACGGGTG	TCCGTCCCAG	120
CTCCGGCCTG	CCAGTGTAGT	TCTACCATCA	TGGACCTATT	GTTCGGGCGC	CGGAAGACGC	180
CAGAGGAGCT	ACTGCGGCAG	AACCAGAGGG	CCCTGAACCG	TGCCATGCGG	GAGCTGGACC	240
CGGAGCGACA	GAAACTTAGAG	ACCCAGGAGA	AGAAAAATCT	TGCAGACATT	AAGAAGATGG	300
CCAAGCAAGG	CCAGATGGAT	GCTGTTTCGCA	TCATGGCAA	AGACTTGGTG	CGCACCCGGC	360
GCTATGTGCG	CAAGTTTGTA	TTGATGCGGG	CCAACATCCA	GGCTGTGTCC	CTCAAGATCC	420
AGACACTCAA	GTCCAACAAC	TCGATGGCAC	AAGCCATGAA	GGGTGTCAAC	AAGGCCATGG	480
GCACCATCAA	CAGACAGCTG	AAGTTGCCCC	AGATCCAGAA	GATCATGATG	GAGTTTGGAG	540
GCAGGCAGA	GATCATGGAT	ATGAAGGAGA	AGATGATGAA	TGATGCCATT	GATGATCCCA	600
TGGGTGATGA	GGAAGATGAA	GAGGAGAGTG	ATGCTGTGGT	GTCCCAGGTT	CTGGATGAGC	660
TGGGACTTAG	CCTAACAGAT	GAGCTGTCTGA	ACCTCCCCTC	AAC TGGGGGC	TCGCTTAGTG	720
TGGCTGTGTG	TGGGAAAAAA	GCAGAGGCCG	CAGCCTCAGC	CCTAGCTGAT	GCTGATGCAG	780
ACCTGGAGTA	ACGGCTTAAG	AACCTGCGGA	GGGACTGAGT	GGCCCTGCCA	CTCCGAGATA	840
ACCAAGTGAT	GCCCGAGATC	TTTTACCACA	ACCCTCTGT	AATAAAAGAG	ATTTGACACT	900

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1145 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```

GGGCCCCGCC CAGGCGGCTG CCCGTGACCT GCCTGGGCGC GGGGAAGTGA AAGCCGGAAG 60
GGGCAAGACG GGTTCAGTTC GTCATGGGGC TGTTTGGAAA GACCCAGGAG AAGCCGCCCCA 120
AAGAAGTGGT CAATGAGTGG TCATTGAAGA TAAGAAAGGA AATGAGAGTT GTTGACAGGC 180
AAATAAGGGA TATCCAAAGA GAAGAAGAAA AAGTGAAACG ATCTGTGAAA GATGCTGCCA 240
AGAAGGGCCA GAAGGATGTC TGCATAGTTC TGGCCAAGGA GATGATCAGG TCAAGGAAGG 300
CTGTGAGCAA GCTGTATGCA TCCAAAGCAC ACATGAACTC AGTGCTCATG GGGATGAAGA 360
ACCAGCTCGC GGTCTTGCGA GTGGCTGGTT CCCTGCAGAA GAGCACAGAA GTGATGAAGG 420
CCATGCAAAG TCTTGTGAAG ATTCCAGAGA TTCAGGCCAC CATGAGGGAG TTGTCCAAAG 480
AAATGATGAA GGCTGGGATC ATAGAGGAGA TGTTAGAGGA CACTTTTGAA AGCATGGACG 540
ATCAGGAAGA AATGGAGGAA GAAGCAGAAA TGGAAATTGA CAGAATTCTC TTTGAAATTA 600
CAGCAGGGGC CTTGGGCAAA GCACCCAGTA AAGTGACTGA TGCCCTTCCA GAGCCAGAAC 660
CTCCAGGAGC GATGGCTGCC TCAGAGGATG AGGGGGAGGA GGAAGAGGCT CTGGAGGCCA 720
TGCAGTCCCG GCTGGCCACA CTCCGCAGCT AGGGGCTGCC TACCCCGCTG GGTGTGCAC 780
CACTCCTCTC AAGAGCTGCC ATTTTATGTG TCTCTGCAC TACACCTCTG TTGTGAGGAC 840
TACCATTTTG GAGAAGGTTT TGTGTGCTC TTTTCATTCT CTGCCCAGGT TTTGGGATCG 900
CAAAGGGATT GTTCTTATAA AAGTGGCATA AATAAATGCA TCATTTTATG GAGTATAGAC 960
AGATATATCT TATTGTGGGG AGGGGAAAGA AATCCATCTG CTCATGAAGC ACTTCTGAAA1020
ATATAGGTGA TTGCCTGAAT GTCGAAGACT CTACTTTTGT CTATAAAACA CTATATAAAT1080
GAATTTTAAT AAATTTTTCG TTTAGCACTT GGCCCCATTG TAGATTGCCG TGTGCAGTAA1140
ACTTT
1145

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(2) INFORMATION ON SEQ ID NO. 270:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1836 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

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GTTGCGACAT GCAGTGCGCC GGAGGAACTG TGCTCTTTGA GGCCGACGCT AGGGGCCCCG 60
AAGGGAAACT GCGAGGCGAA GGTGACCGGG GACCGAGCAT TTCAGATCTG CTCGGTAGAC 120
CTGGTGCAAC ACCACCATGT TGGCTGCAAG GCTGGTGTGT CTCCGGACAC TACCTTCTAG 180
GGTTTTCCAC CCAGCTTTCA CCAAGGCCTC CCCTGTTGTG AAGAATTCCA TCACGAAGAA 240
TCAATGGCTG TTAACACCTA GCAGGGAATA TGCCACCAA ACAAGAATTG GGATCCGGCG 300
TGGGAGAACT GGCCAAGAAC TCAAAGAGGC AGCATTGGAA CCATCGATGG AAAAAATATT 360
TAAATTTGAT CAGATGGGAA GATGGTTTGT TGCTGGAGGG GCTGCTGTTG GTCTTGGAGC 420
ATTGTGCTAC TATGGCTTGG GACTGTCTAA TGAGATTGGA GCTATTGAAA AGGCTGTAAT 480
TTGGCCTCAG TATGTCAAGG ATAGAATTCA TTCCACCTAT ATGTACTTAG CAGGGAGTAT 540
TGGTTTAAAC GCTTTGTCTG CCATAGCAAT CAGCAGAACG CCTGTTCTCA TGAACCTCAT 600
GATGAGAGGC TCTTGGGTGA CAATTGGTGT GACCTTTGCA GCCATGGTTG GAGCTGGAAT 660
GCTGGTACGA TCAATACCAT ATGACCAGAG CCCAGGCCCA AAGCATCTTG CTTGGTTGCT 720
ACATTCTGGT GTGATGGGTG CAGTGGTGGC TCCTCTGACA ATATTAGGGG GTCCTCTTCT 780
CATCAGAGCT GCATGGTACA CAGCTGGCAT TGTGGGAGGC CTCTCCACTG TGGCCATGTG 840
TGCGCCCACT GAAAAGTTTC TGAACATGGG TGCACCCCTG GGAGTGGGCC TGGGTCTCGT 900
CTTTGTGTCC TCATTGGGAT CTATGTTTCT TCCACCTACC ACCGTGGCTG GTGCCACTCT 960
TTACTCAGTG GCAATGTACG GTGGATTAGT TCTTTTCAGC ATGTTCTTTC TGTATGATAC1020
CCAGAAAGTA ATCAAGCGTG CAGAAGTATC ACCAATGTAT GGAGTTCAAA AATATGATCC1080
CATTAACCTG ATGCTGAGTA TCTACATGGA TACATTAAAT ATATTTATGC GAGTTGCAAC1140
TATGCTGGCA ACTGGAGGCA ACAGAAAGAA ATGAAGTGAC TCAGCTTCTG GCTTCTCTGC1200
TACATCAAAAT ATCTTGTTTA ATGGGGCAGA TATGCATTAA ATAGTTTGTA CAAGCAGCTT1260
TCGTTGAAGT TTAGAAGATA AGAAACATGT CATCATATTT AAATGTTCCG GTAATGTGAT1320
GCCTCAGGTC TGCCTTTTTT TCTGGAGAAT AAATGCAGTA ATCCTCTCCC AAATAAGCAC1380
ACACATTTTC AATTCTCATG TTTGAGTGAT TTTAAATGT TTTGGTGAAT GTGAAAATA1440
AAGTTTGTGT CATGAGAATG TAAGTCTTTT TTCTACTTTA AAATTTAGTA GGTTCAGTGA1500
GTAACAAAAA TTTAGCAAAC CTGTGTTTGC ATATTTTTTT GGAGTGCAGA ATATTGTAAT1560
TAATGTCATA AGTGATTTGG AGCTTTGGTA AAGGGACCAG AGAGAAGGAG TCACCTGCAG1620
TCTTTTGTGT TTTTAAATAC TTAGAACTTA GCACCTGTGT TATTGATTAG TGAGGAGCCA1680
GTAAGAAACA TCTGGGTATT TGGAAACAAG TGGTCATTGG TTACATTCAT CTGCTGAACT1740
TAACAAAACT GGTTCCATCC TGGAACAGGG CACAGGTGAA TGCATTCTC CTGCGGTTGG1800
CTCCCCAGTG GCGCGCCTTC CCATATAGGA TGTGGG 1836

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(2) INFORMATION ON SEQ ID NO. 271:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 1220 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

1220

(2) INFORMATION ON SEQ ID NO. 272:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1303 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

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CGCAGTGCGC AGGCGTGGGG CTCTCTCCTT GTCAGTCGGC GCCGCGTGCG GGCTGGTGGC 60
TCTGTGGCAG CGGCGGCGGC AGGACTCCGG CACTATGAGC GGCTTCAGCA CCGAGGAGCG 120
CGCCGCGCCC TTCTCCCTGG AGTACCGAGT CTTCCTCAA AATGAGAAAG GACAATATAT 180
ATCTCCATTT CATGATATTC CAATTTATGC AGATAAGGAT GTGTTTCACA TGGTAGTTGA 240
AGTACCACGC TGGTCTAATG CAAAAATGGA GATTGCTACA AAGGACCCTT TAAACCCTAT 300
TAAACAAGAT GTGAAAAAAG GAAACTTCG CTATGTTGCG AATTTGTTCC CGTATAAAGG 360
ATATATCTGG AACTATGGTG CCATCCCTCA GACTTGGGAA GACCCAGGGC ACAATGATAA 420
ACATACTGGC TGTTGTGGTG ACAATGACCC AATTGATGTG TGTGAAATTG GAAGCAAGGT 480
ATGTGCAAGA GGTGAAATAA TTGGCGTGAA AGTTCTAGGC ATATTGGCTA TGATTGACGA 540
AGGGGAAACC GACTGGAAAG TCATTGCCAT TAATGTGGAT GATCCTGATG CAGCCAATTA 600
TAATGATATC AATGATGTCA AACGGCTGAA ACCTGGCTAC TTAGAAGCTA CTGTGGACTG 660
GTTTAGAAGG TATAAGGTTT CTGATGGAAA ACCAGAAAAT GAGTTTGCGT TTAATGCAGA 720
ATTTAAAGAT AAGGACTTTG CCATTGATAT TATTAAAAGC ACTCATGACC ATTGGAAAGC 780
ATTAGTGACT AAGAAAACGA ATGGAAGAGG AATCAGTTGC ATGAATACAA CTTTGTCTGA 840
GAGCCCCTTC AAGTGTGATC CTGATGCTGC CAGAGCCATT GTGGATGCTT TACCACCACC 900
CTGTGAATCT GCCTGCACAG TACCAACAGA CGTGGATAAG TGGTTCCATC ACCAGAAAAA 960
CTAATGAGAT TTCTCTGGAA TACAAGCTGA TATTGCTACA TCGTGTTCAT CTGGATGTAT 1020
TAGAAGTAAA AGTAGTAGCT TTCAAAGCT TTAAATTTGT AGAACTCATC TAACTAAAGT 1080
AAATTCTGCT GTGACTAATC CAATATACTC AGAATGTTAT CCATCTAAAG CATTTTTCAT 1140
ATCTCAACTA AGATAACTTT TAGCACATGC TTAAATATCA AAGCAGTTGT CATTTGGAAG 1200
TCACTTGTGA ATAGATGTGC AAGGGGAGCA CATATTGGAT GTATATGTTA CCATATGTTA 1260
GGAAATAAAA TTATTTTGCT GAACTTGGA AAAAAAAA AAA 1303

```

(2) INFORMATION ON SEQ ID NO. 273:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH:** 1586 base pairs
- (B) TYPE:** Nucleic acid
- (C) STRAND:** individual
- (D) TOPOLOGY:** linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM:** HUMAN
- (C) ORGAN:**

(vii) OTHER ORIGIN:

- (A) LIBRARY:** cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

```

CGGCTCGAGC GGCTCGAGAT TCGAGGTCGT GGTGGTCTTG GAAGAGCGTC GAGGGGGCCG 60
TGGACGTGGA ATGGGCCGAG GAGATGGATT TGATTCTCGT GGCAAACGTG AATTGATAG 120
GCATAGTGGA AGTGATAGAT CTGGCCTGAA GCACGAGGAC AAACGTGGAG GTAGCGGATC 180
TCACAACCTGG GGAACGTGCA AAGACGAATT AACAGAGTCC CCCAAATACA TTCAGAAACA 240
AATATCTTAT AATTACAGTG ACTTGGATCA ATCAAATGTG ACTGAGGAAA CACCTGAAGG 300
TGAAGAACAT CATCCAGTGG CAGACACTGA AAATAAGGAG AATGAAGTTG AAGAGGTAAA 360

```

```

AGAGGAGGGT CCAAAAGAGA TGACTTTGGA TGAGTGGAAG GCTATTCAAA ATAAGGACCG 420
GGCAAAAGTA GAATTTAATA TCCGAAAACC AAATGAAGGT GCTGATGGGC AGTGGAGAA 480
GGGATTTGTT CTTTCATAAA CAAAGAGTGA AGAGGCTCAT GCTGAAGATT CGGTTATGGA 540
CCATCATTTT CGGAAGCCAG CAAATGATAT AACGTCTCAG CTGGAGATCA ATTTTGGAGA 600
CCTTGGCCGC CCAGGACGTG GCGGCAGGGG AGGACGAGGT GGACGTGGGC GTGGTGGGCG 660
CCCAAACCGT GGCAGCAGGA CCGACAAGTC AAGTGCTTCT GCTCCTGATG TGGATGACCC 720
AGAGGCATTC CCAGCTCTGG CTTAAGTGA TGCCATAAGA CAACCCTGGT TCCTTTGTGA 780
ACCCTTCTGT TCAAAGCTTT TGCATGCTTA AGGATTCCAA ACGACTAAGA AATTAAGAAA 840
AAAAAGACTG TCATTCATAC CATTACACAC TAAAGACTGA ATTTTATCTG TTTTAAAAAT 900
GAACCTTCTC CGCTACACAG AAGTAACAAA TATGGTAGTC AGTTTTGTAT TTAGAAATGT 960
ATTGGTAGCA GGGATGTTTT CATAATTTTC AGAGATTATG CATTCTTCAT GAATACTTTT 1020
GTATTGCTGC TTGCAAATAT GCATTTCCAA ACTTGAAATA TAGGTGTGAA CAGTGTGTAC 1080
CAGTTTAAAG CTTTCACTTC ATTTGTGTTT TTTAATTAAG GATTTAGAAG TTCCCCCAAT 1140
TACAAACTGG TTTTAAATAT TGGACATACT GGTTTTAATA CCTGCTTTGC ATATTCACAC 1200
ATGGTCAACT GGGACATGTT AAACCTTTGAT TTGTCAAATT TTATGCTGTG TGGAAATACT 1260
ACTATATGTA TTTTAACTTA GTTTTAATAT TTTCATTTT GGGGAAAAAT CTTTTTTCAC 1320
TTCTCATGAT AGCTGTTATA TATATATGCT AAATCTTTAT ATACAGAAAT ATCAGTACTT 1380
GAACAAATTC AAAGCACATT TGGTTTATTA ACCCGTGGCT GCCCTGGCAT GGGGCCCCATT 1440
TGGGGTCCAA ATTATACTG ATTTACATTT TCAGCGATAT TACTTTTAAA TGCCTGAGTT 1500
CCCATTTAAA ATCTAACTAG ACACCTAATG GGGAAGTGGT TAACCACTAT GTGGTAGCCA 1560
CGGGCCAG

```

(2) INFORMATION ON SEQ ID NO. 274:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 144 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

```

KQVKCAKVS Y LLFLFQYCAI DSCIKEFNAG SSWLSSVTLW SMSSVSLSAS NVGRVRIKSE 60
GCSTGDKLSL GVPASKATEP ISFRRSSCS LCCWLSALAS DFFRRSYSGR YLSYSSAAL120
VTCTKSSSNP VPRTAETPTT LSEL

```

(2) INFORMATION ON SEQ ID NO. 275:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 143 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

```
Name: 275          Len: 143  Check: 15DA
MSLVLDEFYS SLRVVGSAV LGTGLDELfV QVTSAAEEYE REYRPEYERL KKSLANAESQ 60
QOREQLERLR KDMGVALDA GTPKDSLSPV LHPSDLILTR PTLEADSDTD DIDHRVTEES120
HEEPAFONFM QESMAQYWKR NNK                                     143
```

(A) LENGTH: 181 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

```
IPNMAAPLGG MFSGQPPGPP QAPPGLPGQA SLLQAAPGAP RPSSSTLVDE LESSFEACFA 60
SLVSQDYVNG TDQEEIRTGV DQCIQKFLDI ARQTECFFLQ KRLQLSVQKP EQVIKEDVSE120
LRNELQRKDA LVQKHLTKLR HWQQVLEDIN VQHKKPADIP QGSLAYLEQA SANIPAPLKP180
T                                     181
```

(A) LENGTH: 89 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

NELIIWQRVL PKCQVHRKEC VANLTHQPTH RPTASALCSR WLQRCRDVGR CLLQVGQGAL60
 RDVGGLFVLH VDVLQHLLPM POLCQVLLD 89

(2) INFORMATION ON SEQ ID NO. 278:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 401 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

MPNFCAAPNC TRKSTQSDLA FFRFPRDPA CQKWVENCRR ADLEDKTFDQ LNKHYRLCAK 60
 HFETSMICRT SPYRTVLRDN AIPTIFDLTS HLNPNHSRHR KRIKELSEDE IRTLKQKKID120
 ETSEQEQQHK ETNNSNAQNP SEEEGEGQDE DILPLTLEEK ENKEYLKSLE EILILMGQN180
 IPLDGHEADE IPEGLFTPDN FQALLECRIN SGEEVLRKRF ETTAVNTLFC SKTQQRQMLE240
 ICESCIREET LREVRDSEHFF SIITDDVVDI AGEHLPVLV RFVDESHNL R EEFIGFLPYE300
 ADAEILAVKF HTMITKWL NMEYCRGQAY IVSSGFSSKM KVVASRLLEK YPQAIYTLCS360
 SCALNMWLAK SVPVMGVSVA LGTIEEVCSF FHXITTTAFR T 401

(2) INFORMATION ON SEQ ID NO. 279:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 106 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

MLISGTLSHG TTQIQYXXEE HHADMYRSDL PNPDTLSAEL HCWRIKWKHR GKDIPLPSTI 60
 YEALHLPDIK FFPNVYALLK VLCILPVMKV ENERYENGTK ASLKHI 106

(2) INFORMATION ON SEQ ID NO. 280:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 398 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

```
GRKCNKFWDN AQTSGIEEPS ETKGSMQKSK FKYKLVPEEE TTASENTEIT SERQKEGIKL 60
TIRISSRKKK PDSPPKVLEP ENKQEKTEKE EEKTNVGRTL RRSRPRISPT AKVAEIRDQK120
ADKKRGEDED EEEEEESTALQ KTDKKEILKK SEKDTNSKVS KVKPKGKVRW TGSRTGRWK180
YSSNDESEGS GSEKSSAASE EEEEEKESEE ILADDDPECK KCGLPNHPPEL ILLCDSCDSG240
YHTACLRPPL MIIPDGEWFC PPCQHKLLCE KLEEQLQDLV VALKKKERAE RRKERLVYVG300
ISIEINIIPPQ EPDFSEDQEE KKKDSKKS KA NLLERRSTRT RKCISYRFDE FDEAIDEAIE360
DDIKEADGGG VGRGKDISTI TGHGKDIST ILDEKIIT 398
```

(2) INFORMATION ON SEQ ID NO. 281:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 198 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

```
SSEKSGSCGG MMFSILIPTY TKRSFLRSAR SFFFKATSKS CNCSSNFSQS SLCWQGGQNH 60
SPSGMIIRGG RRQAVWYPLS QESHRRISG WFGPHFLHG SSSSARMAS LSFSSSSSEA120
ADDFSLPDPS LSSLLEYFHL PRVREPVRT LPLGFTLLTL EFVSFSDFFK ISFLSVFCKA180
VDSSSTSSSP SPLFLSAF 198
```

(2) INFORMATION ON SEQ ID NO. 282:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 202 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

GRLPFSGRGR GKKVTSGDGV ASLPLKLGRL FGGVTRGFNM RIEKCYFCSG PIYPGHGMMF 60
 VRNDCKVFRF CKSKCHKNEK KKRNPVKVRW TKAFRKAAGK ELTVDNSFEF EKRRNEPIKY120
 QRELWNKTID AMKRVEEIKQ KRQAKFIMNR LKKNKELQKV QDIKEVKQNI HLIRAPLAGK180
 GKQLEEKMVQ QLQEDVDMED AP 202

(2) INFORMATION ON SEQ ID NO. 283:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 84 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF**(iii) HYPOTHETICAL: yes****(vi) ORIGIN****(A) ORGANISM: HUMAN****(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:**

IIHCKLFTSC FPECFGPPNF ARIALLFKVF MTRFAKSEH LAIVADEHHA VSRIDGPRTE60
 ITLFDTHVEP ACNPTKQTPK LERK 84

(2) INFORMATION ON SEQ ID NO. 284:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 206 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF**(iii) HYPOTHETICAL: yes****(vi) ORIGIN****(A) ORGANISM: HUMAN****(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:**

RLEPRSVTRS RRAVSRLSAR PGKVSAMAF LASGPYLTHQ QKVLRLYKRA LRHLESWCVQ 60
 RDKYRYFACL MRARFEEHKN EKDMAKATQL LKEAEEEFWY RQHPQPYIFP DSPGGTSYER120
 YDCYKVPWC LDDWHPSEKA MYPDYFAKRE QWKKLRRESW EREVKQLQEE TPPGGPLTEA180
 LPPARKEGDL PPLWWYIVTR PRERP 206

(2) INFORMATION ON SEQ ID NO. 285:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 139 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

PLVPSFPSAV SSTVLSWQSN QDTLPSQKDA SHLSTILGPC SNRISHRRCP QESQGRCAV 60
 DADGTRILPR PPSAAGWPSP YPFHSYVLQT GLSSNKQSIG ICLSGRTTTR GGVAPAYKAA120
 TPFADGSGRV PTPRTPLRR 139

(2) INFORMATION ON SEQ ID NO. 286:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

LMMTIYALSN EFAFKINEEQ LSFFPLLSVQ LWHAQRELLD SWSGVIPFF FSCSCLPFLY60
 PPRWRQIHDL KDTQYLLNSS 80

(2) INFORMATION ON SEQ ID NO. 287:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

LMMTIYALSN EFAFKINEEQ LSFFPLLSVQ LWHAQRFLLD SWSGVIPFF FSCSCLPFLY60
PPKWRQIHD L KDTQYLLNSS 80

(2) INFORMATION ON SEQ ID NO. 288:

(i) SEQUENCE CHARACTERISTIC:

- SEQUENCE CHARACTERISTICS
- (A) LENGTH: 206 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) **HYPOTHETICAL:** yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```

RLSCAGTLSG  SGPHPSRRLT  QGRWVRKSRV  AMEKIPVSAF  LLLVALSYTL  ARDTTVKPGA  60
KKDTKDSRPK  LPQTLSRGWG  DQLIWTQTYE  EALYKSKTSN  KPLMIHHLD  ECPHSQALKK  120
VFAENKEIQK  LAEQVLLNL  VYETTDKHL  PDGQYVPRIM  FVDPSLTVRA  DITGRYSNRL  180
YAYEPADTAL  LLDNMKKALK  LLKTEL
                                                    206

```

(2) INFORMATION ON SEQ ID NO. 289:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 77 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) **HYPOTHETICAL:** yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

GNPELPWRKF QCQHSCSLWP SPTLWPEIQ SNLEPKRTQR TLDPNCPRPS PEVGVTNSSG60
LRHMKKLYIN PRQATNP 77

(2) INFORMATION ON SEQ ID NO. 290:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GGXGXQLLXP XAXQGXPAA S CXXQDVHLXR CXTVVRWYQR ITGMPXXAPT RNFSKFQRXV 60
 MDLHGFPKEX GXEXQEXLQ WEGRSSSGKC RISXSXLPXS TIXXFLKXXW XXIRXQSPXT120
 WXRTYLR LGS ISEFSPGSCL PNWLEGKPRM TXAKWPKFFL 160

(2) INFORMATION ON SEQ ID NO. 291:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

RHXPLXLGXH GHRAHSCLGW SOXALWDXAW GLXXXGSXQX RKKEAXWCVX VGXVGXCXXP 60
 XEXMXXGF EQ NXXGPNXXV SXLGXXXWNR XAEKNMXGCC AKXVNXMDH XXGFQXRQIR120
 GLCSHAHTGX NCHVSXSGSD TQLCXGLSFM 150

(2) INFORMATION ON SEQ ID NO. 292:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

RAAKILKGGL QEVAEQLELE RIGPQHQAGS DSLLTGMAFF KMREMFFEDH IDDAKYCGHL60
YGLGSGSSYV QNGTGNAYEE EANKQS 86

(2) INFORMATION ON SEQ ID NO. 293:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 64 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

IKAKFNLNAF FFFFLLRSEI GTVILSTERQ TIKWAMKGGG KVLIVRGIQ PEIKPIYKHV60
CSSK 64

(2) INFORMATION ON SEQ ID NO. 294:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 226 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

ASTIMDLLFG RRKTPEELLR QNQRALNRAM RELDRERQKL ETQEKKIID IKKMAKQGQM 60
DAVRIMAKDL VRTRRYVRKF VLMRANIQAV SLKIOTLKSN NSMAQAMKGV TKAMGTMNRQ120
LKLPIQKIM MEFERQAEIM DMKEEMMND AIDPMGDEED EEESDAVVSQ VLDELGLSLT180
DELSNLPSTG GSLSVAAGGK KAEAAASALA DADADLEERL KNLRRD 226

(2) INFORMATION ON SEQ ID NO. 295:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 166 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

KILGIHWLSR SGRGTQSLRR FLSRSSRSAS ASARAEAAAS AFFPPAATLS EPPVEGRFDS 60
 SSVRLSPSSS RTWDTTASLS SSSSSSPMGS SMASFISSF ISMISACRSN SIMIFWIWGN120
 FSCLEFVPMALVTPEMACAI ELLDLSVWIL RDTAWMLARI NTNLR 166

(2) INFORMATION ON SEQ ID NO. 296:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 233 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

KPEGARRVQF VMGLFGKTQE KPPKELVNEW SLKIRKEMRV VDRQIRDIQR EEEKVKRSVK 60
 DAAKKGQKDV CIVLAKEMIR SRKAVSKLYA SKAHMNSVLM GMKNQLAVLR VAGSLQKSTEL20
 VMKAMQSLVK IPEIQATMRE LSKEMMKAGI IEEMLEDTFE SMDDQEEMEE EAEMEIDRIL180
 FEITAGALGK APSKVTDALP EPEPPGAMAA SEDEGEEEEE LEAMQSRLAT LRS 233

(2) INFORMATION ON SEQ ID NO. 297:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 129 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

LMPFQSQNLQ ERWLPQMRG RRRKRLWRPCS PGWPHSAARG CLPRWVCTHS SQELPFYVSL 60
 ALHLCCEDYH FEGGSVCLFS FSAQVLGSQR DCSYKSGINK CIIFRSIDRY ILLWGGERNP120
 SAHEALLKI 129

(2) INFORMATION ON SEQ ID NO. 298:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 351 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

TWCTTTMLAA RLVCRLTLPs RVFHPAFTKA SPVVKNSITK NQWLLTPSRE YATKTRIGIR 60
 RGR TGQELKE AALEPSMEKI FKIDQMGRWF VAGGA AVGLG ALCYYGLGLS NEIGAIEKAV120
 IWPQYVKDRI HSTYMYLAGS IGLTALSAIA ISRTPVLMNF MMRG SWVTIG VTFAAMVGAG180
 MLVRSIPYDQ SPGPKHLAWL LHSGVMGAVV APLTILGGPL LIRAAWYTAG IVGGLSTVAM240
 CAPSEKFLNM GAPLGVGLGL VEVSSLGSMF LPPTTVAGAT LYSVAMYGGL VLFSMFLLYD300
 TQKVIKRAEV SPMYGVQKYD PINSMLSIYM DTLNIFMRVA TMLATGGNRK K 351

(2) INFORMATION ON SEQ ID NO. 299:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 147 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

RVAPATVVGG RNIDPNEDTK TRPRPTPRGA PMERNFSLGA HMATVERPPT MPAVYHAALM 60
 RRGPPNIVRG ATTAPITPEC SNQARCFGPG LWSYGIDRTS IPAPTMAAKV TPIVTQEPLI120
 MKFMRTGVLL IAMADKAVKP ILPAKYI 147

(2) INFORMATION ON SEQ ID NO. 300:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 188 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

RRLEVSRYQH HFRVSLAPWS KMADEATRRV VSEIPVLKTN AGPRDRELWV QRLKEEYQSL 60
 IRYVENNKNA DNDWFRLESN KEGTRWFGKC WYIHDLLKYE FDIEFDIPIT YPTTAPEIAV120
 PELDGKTAKM YRGGKICLTD HFKPLWARNV PKFGLAHLMA LGLGPWLAVE IPDLIQKGV180
 QHKEKCNQ 188

(2) INFORMATION ON SEQ ID NO. 301:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 172 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

SKFGHIPGPO RFEMIRQAYF ATPVHLCCLS IQLRNCNFWG SSRICDRNVK LDVKLIFQEV 60
 MDIPAFSKPP SSFLVGLQSE PIVVSILVVL HIPDKGLIFL LQSLHPQLTI SGSGVSLQHR120
 DLRHNTSRGF IRHLGPGRKR NAEVVLPVAY LKAPSSLLWE DETLGCKTS FE 172

(2) INFORMATION ON SEQ ID NO. 302:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 320 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

AVRRRGALSL SVGAACGLVA LWQRRRQDSG TMSGFSTEER AAPFSLEYRV FLKNEKGQYI 60
 SPFHDIPIYA DKDVFHVVVE VPRWSNAKME IATKDPLNPI KQDVKKGKLR YVANLFPYKG120
 YIWNYGAIPQ TWEDPGHNDK HTGCCGDNDP IDVCEIGSKV CARGEIIGVK VLGILAMIDE180
 GETDWKVIAT NVDDPDAAANY NDINDVKRLK PGYLEATVDW FRRYKVPDGG PENEFAFNAE240
 FKDKDFAIDI IKSTHDHWKA LVTKKTNGKG ISCMNTTISE SPFKCDPDAA RAIVDALPPP300
 CESACTVPTD VDKWFHHQKN 320

(2) INFORMATION ON SEQ ID NO. 303:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

RVLCSNLHFC IRPAWYFNYH VKHILICINW NIMKWRYILS FLIFEEDSVL QGEGRGALLG60
 AEAHSAGVL PPPLPQSHQP ARGAD 85

(2) INFORMATION ON SEQ ID NO. 304:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 247 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

GSSGSRFEVV VVLEERRGGR GRGMGRGDGF DSRGKREFDR HSGSDRSLK HEDKRGGSGS 60
 HNWTGTVKDEL TESPKEYIQKQ ISYNYSDLDQ SNVTEETPEG EEHHPVADTE NKENEVEEVK120
 EEGPKEMTLD EWKAIQNKDR AKVEFNIRKP NEGADGQWKK GFVLHKSSE EAAHEDSVMD180
 HHFRKPANDI TSQLEINFGD LGRPGRGGGR GRGGRGRGR PNRGSRTDKS SASAPDVDDP240
 EAFPALA 247

(2) INFORMATION ON SEQ ID NO. 305:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

SFGILKHAKA LNRRVHKGTR VVLWHPVKPE LGMPLGHPHQ EQKHLTCRSC CHGLGAHHAH60
 VHLVLPCHRV LGGQGLQN 78

(2) INFORMATION ON SEQ ID NO. 306:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 293 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

ATRGAEQDGG ASAARPRRRW AGGLLQRAAP CSLLPRLRTW TSSSNRSRED SWLKSLEVRK 60
 VDPRKDAHSN LLAKKETSNI YKLQFHNVPK ECLEAYNKIC QEVLPKIHED KHYPCTLVGT120
 WNTWYGEQDQ AVHLWRYEGG YPALTEVMNK LRENKEFLEF RKARSDMLLS RKNQLLLEFS180
 FWNEPVPRSG PNIYELRSYQ LRPGMTIEWG NYWARAIRFR QDGNEAVGGF FSQIGQLYMV240
 HHLWAYRDLQ TREDIRNAAW HKHGWEELVY YTVPLIQEME SRIMIPLKTS PLQ 293

(2) INFORMATION ON SEQ ID NO. 307:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 208 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

AHRNSTALLE GRGLQWDHDS GFHFLNKWNC VIYQFLPAMF VPCCIPYVFP GLKIPVSPKM 60
 VHHVQLPNLR EESSDGFVTI LSEADCTSPV IAPFNHGSWS ELVRPEFIYI RSGSWHRLIP120
 ETELQOELIL PGEKHVTSC LTKFQKFLIFS EFIHDFCEGW IASFIPPEVD SLVLLAIPRV180
 PSPHQSTRVV FIFVNLWQHL LTNFVVC F 208